GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:31:07 ; Search time 30 Seconds
(without alignments)
37.025 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 135323

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	10	22	AAB46225	Human APP derived
2	52	94.5	10	22	AAB82641	All-D peptide used
3	50	90.9	9	22	AAB48493	Antifibrillogenic
4	50	90.9	10	22	AAB46224	Human APP derived
5	47	85.5	10	22	AAB46226	Human APP derived
6	46	83.6	8	18	AAW45937	Amyloid beta pepti
7	46	83.6	9	18	AAW45935	Amyloid beta pepti
8	46	83.6	10	18	AAW45934	Amyloid beta pepti
9	46	83.6	10	22	AAB46223	Human APP derived
10	42	76.4	8	17	AAW02310	Beta-amyloid modul
11	42	76.4	8	20	AAW89374	Beta-amyloid pepti
12	40	72.7	7	18	AAW45941	Amyloid beta pepti
13	40	72.7	8	18	AAW45938	Amyloid beta pepti
14	40	72.7	9	18	AAW45936	Amyloid beta pepti
15	40	72.7	10	22	AAB46222	Human APP derived
16	39	70.9	10	22	AAB46227	Human APP derived
17	38	69.1	7	14	AAR45231	Beta amyloid prote
18	38	69.1	7	17	AAW02311	Beta-amyloid modul
19	38	69.1	7	18	AAW45940	Amyloid beta pepti
20	38	69.1	7	20	AAW89375	Beta-amyloid pepti
21	36	65.5	9	14	AAR45239	Mutant amyloid pre
22	34	61.8	6	18	AAW45946	Amyloid beta pepti
23	34	61.8	7	14	AAR45232	Beta amyloid prote
24	34	61.8	7	16	AAR87921	Test peptide used
25	34	61.8	7	16	AAR88300	Non-amnestic pepti
26	34	61.8	7	16	AAR80370	Protein polymeric
27	34	61.8	7	17	AAW02312	Beta-amyloid modul
28	34	61.8	7	18	AAW45942	Amyloid beta pepti
29	34	61.8	7	19	AAW49755	Glutamine donor pe
30	34	61.8	7	20	AAW89376	Beta-amyloid pepti
31	34	61.8	7	22	AAB67281	Residues 16-22 of
32	34	61.8	8	18	AAW45939	Amyloid beta pepti
33	34	61.8	8	18	AAW32551	Amyloidogenic sequ
34	34	61.8	8	22	AAE10663	Human amyloid prec
35	34	61.8	8	22	AAE02615	Human amyloid prec
36	34	61.8	10	21	AAY79938	Beta-amyloid recog
37	34	61.8	10	22	AAB46221	Human APP derived
38	34	61.8	10	22	AAB46228	Human APP derived
39	32	58.2	6	18	AAW45945	Amyloid beta pepti
40	31	56.4	7	14	AAR45233	Beta amyloid prote
41	31	56.4	7	22	AAB82639	All-D peptide used
42	31	56.4	7	22	AAB82640	All-D peptide used
43	31	56.4	7	22	AAB48491	Antifibrillogenic
44	31	56.4	7	22	AAB48492	Antifibrillogenic
45	30	54.5	5	18	AAW45952	Amyloid beta pepti
46	30	54.5	6	17	AAW02313	Beta-amyloid modul
47	30	54.5	6	18	AAW45947	Amyloid beta pepti
48	30	54.5	6	18	AAW45944	Amyloid beta pepti
49	30	54.5	6	20	AAY39801	Beta-amyloid prote
50	30	54.5	6	20	AAW29090	A-beta-binding pep

ALIGNMENTS

RESULT 1
AAB46225
ID AAB46225 standard; peptide; 10 AA.
XX
AC AAB46225;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #21.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.

pdafter 11-29-00 Pub WO/00 72880
earlier priority by 9 months

XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 1 HHQKLVFFAE 10

RESULT 2
AAB82641
ID AAB82641 standard; Peptide; 10 AA.
XX
AC AAB82641;
XX
DT 02-OCT-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease;
KW vaccine; therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..10
FT /note= "all D-form residues"
XX
PN WO200139796-A2.
XX
PD 07-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-CA01413.
XX
PR 29-NOV-1999; 99US-0168594.
PR 28-NOV-2000; 2000US-0724842.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Chalifour R, Hebert L, Kong X, Gervais F;
XX
DR WPI; 2001-441458/47.
XX
PT Preventing/treating amyloid-related disease, especially Alzheimer's
PT disease, comprises administering antigenic all-D peptide, e.g. as
PT vaccine, which elicits production of antibodies to prevent
PT fibrillogenesis and associated cellular toxicity -
XX
PS Disclosure; Page 11; 31pp; English.
XX
CC The present sequence is that of an all-D peptide suitable for
CC use in preparing vaccines for preventing or treating Alzheimer's
CC disease and other amyloid related disorders in humans. It is based
CC on a portion of amyloid-beta peptide (see AAB82622), and may be
CC modified by removing or inserting 1 or more amino acid residues, or
CC by substituting 1 or more amino acid residues with other amino acid
CC residues or non-amino acid fragments. Vaccines of the invention
CC are produced using 'non-self' peptides synthesised from the
CC unnatural D-configuration amino acids to avoid the drawbacks of
CC 'self' proteins. The all-D peptides need not be aggregated to be
CC operative or immunogenic. They preferably interact with at
CC least 1 region of an amyloid protein, e.g. the beta-sheet region
CC or GAG-binding site region, the amyloid-beta peptide, or their
CC immunogenic fragments, protein conjugates, immunogenic derivative
CC peptides and immunogenic peptidomimetics. Examples include all-D
CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
CC derivative peptides given in AAB82623-64. The vaccine elicits a
CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and
CC associated cellular toxicity. The amyloid related diseases may be
CC localised amyloidosis, e.g. diabetes type II, neurodegenerative
CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
CC disease, scrapie, cerebral amyloid angiopathy, and prion protein
CC related disorders, or systemic amyloidosis associated with chronic
CC infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and
CC systemic amyloidosis found in long-term haemodialysis patients.
XX
SQ Sequence 10 AA;

Query Match 94.5%; Score 52; DB 22; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.00056;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
|||||||||:
Db 1 HHQKLVFFAQ 10

RESULT 3
AAB48493
ID AAB48493 standard; Peptide; 9 AA.
XX
AC AAB48493;
XX
DT 02-MAR-2001 (first entry)
XX
DE Antifibrillogenic peptide #20.
XX
KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /note= "C-terminal amide"
XX
PN WO200068263-A2.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-CA00515.
XX
PR 05-MAY-1999; 99US-0132592.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Chalifour R, Gervais F, Gupta A;
XX
DR WPI; 2001-031852/04.
XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic -
XX
PS Claim 7; Page 25; 46pp; English.
XX
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are
CC therefore useful for treating amyloidosis disorders such as Alzheimer's
CC disease. Peptides AAB48474-B48496 were identified from the
CC glycosaminoglycan binding region and the prot-prot interaction region of
CC the human amyloid protein.
XX
SQ Sequence 9 AA;

Query Match 90.9%; Score 50; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
|||||||||
Db 1 HHQKLVFFA 9

RESULT 4
AAB46224
ID AAB46224 standard; peptide; 10 AA.
XX
AC AAB46224;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #20.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
|||||||||
Db 2 HHQKLVFFA 10

RESULT 5
AAB46226
ID AAB46226 standard; peptide; 10 AA.
XX
AC AAB46226;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #22.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 85.5%; Score 47; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFFAE 10
|||||||||
Db 1 HQKLVFFAE 9

```
RESULT 6
AAW45937
ID   AAW45937 standard; peptide; 8 AA.
XX
AC   AAW45937;
XX
DT   30-JUN-1998  (first entry)
XX
DE   Amyloid beta peptide fragment.
XX
KW   Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW   positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS   Homo sapiens.
XX
PN   WO9721728-A1.
XX
PD   19-JUN-1997.
XX
PF   09-DEC-1996;   96WO-SE01621.
XX
PR   29-DEC-1995;   95US-0009386.
PR   12-DEC-1995;   95SE-0004467.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Naslund J,  Nordstedt C,  Terenius L,  Thyberg J,  Tjernberg LO;
XX
DR   WPI; 1997-332723/30.
XX
PT   Use of new and known peptide(s) for inhibition of polymerisation of
PT   amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT   Down's syndrome associated with amyloidosis.
XX
PS   Example 1; Figure 2B; 31pp; English.
XX
CC   This sequence represents a fragment of the amyloid beta peptide. The
CC   invention relates to the use of peptide compounds for inhibition of
CC   polymerisation of amyloid beta peptide (ABP), as model substances for
CC   synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC   tool for the identification of other organic compounds with similar
CC   functional properties, or as ligands in positron emission tomography.
CC   The peptides may be used in treatment of amyloidosis, especially in
CC   treatment of Alzheimer's disease associated with amyloidosis, for
CC   treatment or prevention of demens in patients with Down's syndrome, for
CC   treatment or prevention of hereditary cerebral haemorrhage with
CC   amyloidosis (Dutch type) or for the prevention of fibril formation of
CC   human amyloid protein. They can also be used for identifying other
CC   molecules with similar properties and/or as ligands for detection of
CC   amyloid deposits using e.g. positron emission tomography.
XX
SQ   Sequence   8 AA;

  Query Match             83.6%;  Score 46;  DB 18;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFF 8
          ||||||||
Db      1 HHQKLVFF 8


RESULT 7
AAW45935
ID   AAW45935 standard; peptide; 9 AA.
XX
AC   AAW45935;
XX
DT   08-JUL-1998  (first entry)
XX
DE   Amyloid beta peptide fragment.
XX
KW   Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW   positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS   Homo sapiens.
XX
PN   WO9721728-A1.
XX
PD   19-JUN-1997.
XX
PF   09-DEC-1996;   96WO-SE01621.
XX
PR   29-DEC-1995;   95US-0009386.
PR   12-DEC-1995;   95SE-0004467.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Naslund J,  Nordstedt C,  Terenius L,  Thyberg J,  Tjernberg LO;
XX
DR   WPI; 1997-332723/30.
XX
PT   Use of new and known peptide(s) for inhibition of polymerisation of
PT   amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT   Down's syndrome associated with amyloidosis.
XX
PS   Example 1; Figure 2B; 31pp; English.
XX
CC   This sequence represents a fragment of the amyloid beta peptide. The
CC   invention relates to the use of peptide compounds for inhibition of
CC   polymerisation of amyloid beta peptide (ABP), as model substances for
CC   synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC   tool for the identification of other organic compounds with similar
CC   functional properties, or as ligands in positron emission tomography.
CC   The peptides may be used in treatment of amyloidosis, especially in
CC   treatment of Alzheimer's disease associated with amyloidosis, for
CC   treatment or prevention of demens in patients with Down's syndrome, for
CC   treatment or prevention of hereditary cerebral haemorrhage with
CC   amyloidosis (Dutch type) or for the prevention of fibril formation of
CC   human amyloid protein. They can also be used for identifying other
CC   molecules with similar properties and/or as ligands for detection of
CC   amyloid deposits using e.g. positron emission tomography.
XX
SQ   Sequence   9 AA;

  Query Match             83.6%;  Score 46;  DB 18;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFF 8
          ||||||||
Db      2 HHQKLVFF 9


RESULT 8
AAW45934
ID   AAW45934 standard; peptide; 10 AA.
XX
AC   AAW45934;
XX
DT   08-JUL-1998  (first entry)
XX
DE   Amyloid beta peptide fragment (residues 11-20).
XX
KW   Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW   positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS   Homo sapiens.
XX
PN   WO9721728-A1.
XX
PD   19-JUN-1997.
XX
PF   09-DEC-1996;   96WO-SE01621.
XX
```

PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Page 10; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide
CC (residues 11-20). The invention relates to the use of peptide
CC compounds for inhibition of polymerisation of amyloid beta peptide
CC (ABP), as model substances for synthesis of ABP-ligands for inhibition
CC of polymerisation of ABP, as a tool for the identification of other
CC organic compounds with similar functional properties, or as ligands in
CC positron emission tomography. The peptides may be used in treatment of
CC amyloidosis, especially in treatment of Alzheimer's disease associated
CC with amyloidosis, for treatment or prevention of demens in patients with
CC Down's syndrome, for treatment or prevention of hereditary cerebral
CC haemorrhage with amyloidosis (Dutch type) or for the prevention of
CC fibril formation of human amyloid protein. They can also be used for
CC identifying other molecules with similar properties and/or as ligands
CC for detection of amyloid deposits using e.g. positron emission
CC tomography.
XX
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFF 8
||||||||
Db 3 HHQKLVFF 10

RESULT 9
AAB46223
ID AAB46223 standard; peptide; 10 AA.
XX
AC AAB46223;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #19.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFF 8
||||||||
Db 3 HHQKLVFF 10

RESULT 10
AAW02310
ID AAW02310 standard; peptide; 8 AA.
XX
AC AAW02310;
XX
DT 02-MAY-1997 (first entry)
XX
DE Beta-amyloid modulator peptide #1.
XX
KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9628471-A1.
XX
PD 19-SEP-1996.
XX
PF 14-MAR-1996; 96WO-US03492.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
XX
PA (PHAR-) PHARM PEPTIDES INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
XX
DR WPI; 1996-433762/43.
XX
PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
PT protein coupled (in)directly to at least 1 modifying gp., useful in
PT treatment of Alzheimer's disease
XX
PS Claim 16; Page 90; 106pp; English.

XX
CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
CC modulator compounds of the invention. Beta-amyloid peptide is a 4
CC kilodalton peptide that is the major protein component of amyloid
CC plaques. Amyloid plaques are present both in the brain lesions, and in
CC the walls of cerebral blood vessels in Alzheimer's disease patients.
CC The amyloid modulators of the invention comprise an amyloidogenic protein
CC or peptide (such as this sequence) coupled directly or indirectly to at
CC least one modifying group. The modifying group is preferably a cyclic,
CC heterocyclic, or polycyclic group, such as declain, a cholanyl group, a
CC biotin containing group, or a fluorescein containing group. These
CC compounds then modulate the aggregation of these sequences to natural
CC amyloid proteins or peptides when contacted with the natural
CC amyloidogenic proteins or peptides. The modulator compounds can be used
CC in the treatment of disorders associated with amyloidosis, such as
CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
CC and other types of amyloidosis. The modulators are also useful for the
CC treatment of disorders associated with beta-amyloidosis, especially
CC Alzheimer's disease.
XX
SQ Sequence 8 AA;

Query Match 76.4%; Score 42; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFFA 9
||||||||
Db 1 HQKLVFFA 8

RESULT 11
AAW89374
ID AAW89374 standard; peptide; 8 AA.
XX
AC AAW89374;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-14-21.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Example 12; Column 64; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 8 AA;

Query Match 76.4%; Score 42; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFFA 9
||||||||
Db 1 HQKLVFFA 8

RESULT 12
AAW45941
ID AAW45941 standard; peptide; 7 AA.
XX
AC AAW45941;
XX
DT 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for

```
CC   treatment or prevention of hereditary cerebral haemorrhage with
CC   amyloidosis (Dutch type) or for the prevention of fibril formation of
CC   human amyloid protein. They can also be used for identifying other
CC   molecules with similar properties and/or as ligands for detection of
CC   amyloid deposits using e.g. positron emission tomography.
XX
SQ   Sequence   7 AA;

  Query Match             72.7%;  Score 40;  DB 18;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVF 7
          |||||||
Db      1 HHQKLVF 7


RESULT 13
AAW45938
ID   AAW45938 standard; peptide; 8 AA.
XX
AC   AAW45938;
XX
DT   30-JUN-1998  (first entry)
XX
DE   Amyloid beta peptide fragment.
XX
KW   Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW   positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS   Homo sapiens.
XX
PN   WO9721728-A1.
XX
PD   19-JUN-1997.
XX
PF   09-DEC-1996;   96WO-SE01621.
XX
PR   29-DEC-1995;   95US-0009386.
PR   12-DEC-1995;   95SE-0004467.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Naslund J,  Nordstedt C,  Terenius L,  Thyberg J,  Tjernberg LO;
XX
DR   WPI; 1997-332723/30.
XX
PT   Use of new and known peptide(s) for inhibition of polymerisation of
PT   amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT   Down's syndrome associated with amyloidosis.
XX
PS   Example 1; Figure 2B; 31pp; English.
XX
CC   This sequence represents a fragment of the amyloid beta peptide. The
CC   invention relates to the use of peptide compounds for inhibition of
CC   polymerisation of amyloid beta peptide (ABP), as model substances for
CC   synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC   tool for the identification of other organic compounds with similar
CC   functional properties, or as ligands in positron emission tomography.
CC   The peptides may be used in treatment of amyloidosis, especially in
CC   treatment of Alzheimer's disease associated with amyloidosis, for
CC   treatment or prevention of demens in patients with Down's syndrome, for
CC   treatment or prevention of hereditary cerebral haemorrhage with
CC   amyloidosis (Dutch type) or for the prevention of fibril formation of
CC   human amyloid protein. They can also be used for identifying other
CC   molecules with similar properties and/or as ligands for detection of
CC   amyloid deposits using e.g. positron emission tomography.
XX
SQ   Sequence   8 AA;

  Query Match             72.7%;  Score 40;  DB 18;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVF 7
          |||||||
Db      2 HHQKLVF 8


RESULT 14
AAW45936
ID   AAW45936 standard; peptide; 9 AA.
XX
AC   AAW45936;
XX
DT   30-JUN-1998  (first entry)
XX
DE   Amyloid beta peptide fragment.
XX
KW   Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW   positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS   Homo sapiens.
XX
PN   WO9721728-A1.
XX
PD   19-JUN-1997.
XX
PF   09-DEC-1996;   96WO-SE01621.
XX
PR   29-DEC-1995;   95US-0009386.
PR   12-DEC-1995;   95SE-0004467.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Naslund J,  Nordstedt C,  Terenius L,  Thyberg J,  Tjernberg LO;
XX
DR   WPI; 1997-332723/30.
XX
PT   Use of new and known peptide(s) for inhibition of polymerisation of
PT   amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT   Down's syndrome associated with amyloidosis.
XX
PS   Example 1; Figure 2B; 31pp; English.
XX
CC   This sequence represents a fragment of the amyloid beta peptide. The
CC   invention relates to the use of peptide compounds for inhibition of
CC   polymerisation of amyloid beta peptide (ABP), as model substances for
CC   synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC   tool for the identification of other organic compounds with similar
CC   functional properties, or as ligands in positron emission tomography.
CC   The peptides may be used in treatment of amyloidosis, especially in
CC   treatment of Alzheimer's disease associated with amyloidosis, for
CC   treatment or prevention of demens in patients with Down's syndrome, for
CC   treatment or prevention of hereditary cerebral haemorrhage with
CC   amyloidosis (Dutch type) or for the prevention of fibril formation of
CC   human amyloid protein. They can also be used for identifying other
CC   molecules with similar properties and/or as ligands for detection of
CC   amyloid deposits using e.g. positron emission tomography.
XX
SQ   Sequence   9 AA;

  Query Match             72.7%;  Score 40;  DB 18;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVF 7
          |||||||
Db      3 HHQKLVF 9


RESULT 15
AAB46222
ID   AAB46222 standard; peptide; 10 AA.
XX
AC   AAB46222;
```

XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #18.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 72.7%; Score 40; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVF 7
|||||||
Db 4 HHQKLVF 10

RESULT 16
AAB46227
ID AAB46227 standard; peptide; 10 AA.
XX
AC AAB46227;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #23.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 70.9%; Score 39; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKLVFFAE 10
||||||||
Db 1 QKLVFFAE 8

RESULT 17
AAR45231
ID AAR45231 standard; Peptide; 7 AA.
XX
AC AAR45231;
XX
DT 20-JUN-1994 (first entry)
XX
DE Beta amyloid protein fragment.
XX
KW Amyloid precursor protein; APP; beta amyloid protein; BAP;
KW detection; Alzheimer's disease; Down's syndrome.
XX
OS Homo sapiens.
XX
PN AU9338358-A.
XX
PD 04-NOV-1993.
XX
PF 03-MAY-1993; 93AU-0038358.
XX
PR 01-MAY-1992; 92US-0877675.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR WPI; 1993-406194/51.
DR N-PSDB; AAQ54259.

XX
PT New mutant forms of amyloid precursor protein - for detecting
PT cpds. that modify activity of enzymes involved in precursor
PT cleavage, also new nucleic acid encoding them
XX
PS Disclosure; Page 34; 66pp; English.
XX
CC Recombinant polypeptides produced using the coding sequences of
CC mutant forms of amyloid precursor proteins comprising from the 5' to
CC the 3' end a sequence encoding a marker and either (1) a sequence
CC encoding the N-terminus of an amyloid precursor protein (APP) up to,
CC but not including, the nucleotides encoding the beta amyloid protein
CC (BAP) domain or (2) the BAP domain; or the two ligated together, can
CC be used to detect drugs or compounds that inhibit/augment the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments (deposition of which occurs in patients with Alzheimers
CC disease and Down's syndrome). This fragment corresponding to amino
CC acid residues 14-20 of BAP can be altered and affect the level of
CC secretion of APP's containing the BAP sequence.
XX
SQ Sequence 7 AA;

Query Match 69.1%; Score 38; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFF 8
|||||||
Db 1 HQKLVFF 7

RESULT 18
AAW02311
ID AAW02311 standard; peptide; 7 AA.
XX
AC AAW02311;
XX
DT 02-MAY-1997 (first entry)
XX
DE Beta-amyloid modulator peptide #2.
XX
KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9628471-A1.
XX
PD 19-SEP-1996.
XX
PF 14-MAR-1996; 96WO-US03492.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
XX
PA (PHAR-) PHARM PEPTIDES INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
XX
DR WPI; 1996-433762/43.
XX
PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
PT protein coupled (in)directly to at least 1 modifying gp., useful in
PT treatment of Alzheimer's disease
XX
PS Claim 16; Page 90; 106pp; English.
XX
CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
CC modulator compounds of the invention. Beta-amyloid peptide is a 4
CC kilodalton peptide that is the major protein component of amyloid
CC plaques. Amyloid plaques are present both in the brain lesions, and in
CC the walls of cerebral blood vessels in Alzheimer's disease patients.
CC The amyloid modulators of the invention comprise an amyloidogenic protein
CC or peptide (such as this sequence) coupled directly or indirectly to at
CC least one modifying group. The modifying group is preferably a cyclic,
CC heterocyclic, or polycyclic group, such as declain, a cholanyl group, a
CC biotin containing group, or a fluorescein containing group. These
CC compounds then modulate the aggregation of these sequences to natural
CC amyloid proteins or peptides when contacted with the natural
CC amyloidogenic proteins or peptides. The modulator compounds can be used
CC in the treatment of disorders associated with amyloidosis, such as
CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
CC and other types of amyloidosis. The modulators are also useful for the
CC treatment of disorders associated with beta-amyloidosis, especially
CC Alzheimer's disease.
XX
SQ Sequence 7 AA;

Query Match 69.1%; Score 38; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFF 8
|||||||
Db 1 HQKLVFF 7

RESULT 19
AAW45940
ID AAW45940 standard; peptide; 7 AA.
XX
AC AAW45940;
XX
DT 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The

CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 7 AA;

Query Match 69.1%; Score 38; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFF 8
|||||||
Db 1 HQKLVFF 7

RESULT 20
AAW89375
ID AAW89375 standard; peptide; 7 AA.
XX
AC AAW89375;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-14-20.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Example 12; Column 64; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 7 AA;

Query Match 69.1%; Score 38; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFF 8
|||||||
Db 1 HQKLVFF 7

RESULT 21
AAR45239
ID AAR45239 standard; Peptide; 9 AA.
XX
AC AAR45239;
XX
DT 20-JUN-1994 (first entry)
XX
DE Mutant amyloid precursor protein fragment.
XX
KW Amyloid precursor protein; APP; beta amyloid protein; BAP;
KW detection; Alzheimer's disease; Down's syndrome.
XX
OS Homo sapiens.
XX
PN AU9338358-A.
XX
PD 04-NOV-1993.
XX
PF 03-MAY-1993; 93AU-0038358.
XX
PR 01-MAY-1992; 92US-0877675.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR WPI; 1993-406194/51.
DR N-PSDB; AAQ54267.
XX
PT New mutant forms of amyloid precursor protein - for detecting
PT cpds. that modify activity of enzymes involved in precursor
PT cleavage, also new nucleic acid encoding them
XX
PS Disclosure; Page 35; 66pp; English.
XX
CC Recombinant polypeptides produced using the coding sequences of
CC mutant forms of amyloid precursor proteins comprising from the 5' to
CC the 3' end a sequence encoding a marker and either (1) a sequence
CC encoding the N-terminus of an amyloid precursor protein (APP) up to,
CC but not including, the nucleotides encoding the beta amyloid protein
CC (BAP) domain or (2) the BAP domain; or the two ligated together, can
CC be used to detect drugs or compounds that inhibit/augment the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments (deposition of which occurs in patients with Alzheimers
CC disease and Down's syndrome). This is a fragment of amyloid
CC precursor protein containing a mutation which is associated with
CC diseases involving BAP deposition.
XX
SQ Sequence 9 AA;

Query Match 65.5%; Score 36; DB 14; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.4e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      3 QKLVFFAE 10
          |||||||:
Db      1 QKLVFFAQ 8


RESULT 22
AAW45946
ID   AAW45946 standard; peptide; 6 AA.
XX
AC   AAW45946;
XX
DT   30-JUN-1998  (first entry)
XX
DE   Amyloid beta peptide fragment.
XX
KW   Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW   positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS   Homo sapiens.
XX
PN   WO9721728-A1.
XX
PD   19-JUN-1997.
XX
PF   09-DEC-1996;   96WO-SE01621.
XX
PR   29-DEC-1995;   95US-0009386.
PR   12-DEC-1995;   95SE-0004467.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Naslund J,  Nordstedt C,  Terenius L,  Thyberg J,  Tjernberg LO;
XX
DR   WPI; 1997-332723/30.
XX
PT   Use of new and known peptide(s) for inhibition of polymerisation of
PT   amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT   Down's syndrome associated with amyloidosis.
XX
PS   Example 1; Figure 2B; 31pp; English.
XX
CC   This sequence represents a fragment of the amyloid beta peptide. The
CC   invention relates to the use of peptide compounds for inhibition of
CC   polymerisation of amyloid beta peptide (ABP), as model substances for
CC   synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC   tool for the identification of other organic compounds with similar
CC   functional properties, or as ligands in positron emission tomography.
CC   The peptides may be used in treatment of amyloidosis, especially in
CC   treatment of Alzheimer's disease associated with amyloidosis, for
CC   treatment or prevention of demens in patients with Down's syndrome, for
CC   treatment or prevention of hereditary cerebral haemorrhage with
CC   amyloidosis (Dutch type) or for the prevention of fibril formation of
CC   human amyloid protein. They can also be used for identifying other
CC   molecules with similar properties and/or as ligands for detection of
CC   amyloid deposits using e.g. positron emission tomography.
XX
SQ   Sequence   6 AA;

  Query Match             61.8%;  Score 34;  DB 18;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLV 6
          ||||||
Db      1 HHQKLV 6


RESULT 23
AAR45232
ID   AAR45232 standard; Peptide; 7 AA.
XX
AC   AAR45232;
XX
DT   20-JUN-1994  (first entry)
XX
DE   Beta amyloid protein fragment.
XX
KW   Amyloid precursor protein; APP; beta amyloid protein; BAP;
KW   detection; Alzheimer's disease; Down's syndrome.
XX
OS   Homo sapiens.
XX
PN   AU9338358-A.
XX
PD   04-NOV-1993.
XX
PF   03-MAY-1993;   93AU-0038358.
XX
PR   01-MAY-1992;   92US-0877675.
XX
PA   (AMCY ) AMERICAN CYANAMID CO.
XX
PI   Jacobsen JS,  Vitek MP;
XX
DR   WPI; 1993-406194/51.
DR   N-PSDB; AAQ54260.
XX
PT   New mutant forms of amyloid precursor protein - for detecting
PT   cpds. that modify activity of enzymes involved in precursor
PT   cleavage, also new nucleic acid encoding them
XX
PS   Disclosure; Page 34; 66pp; English.
XX
CC   Recombinant polypeptides produced using the coding sequences of
CC   mutant forms of amyloid precursor proteins comprising from the 5' to
CC   the 3' end a sequence encoding a marker and either (1) a sequence
CC   encoding the N-terminus of an amyloid precursor protein (APP) up to,
CC   but not including, the nucleotides encoding the beta amyloid protein
CC   (BAP) domain or (2) the BAP domain; or the two ligated together, can
CC   be used to detect drugs or compounds that inhibit/augment the
CC   activity of proteolytic enzymes which cleave APP to generate BAP
CC   fragments (deposition of which occurs in patients with Alzheimers
CC   disease and Down's syndrome). This fragment corresponding to amino
CC   acid residues 14-20 of BAP has been altered and APP's containing
CC   the altered BAP sequence show 0% secretion compared with those
CC   containing the wild type BAP sequence.
XX
SQ   Sequence   7 AA;

  Query Match             61.8%;  Score 34;  DB 14;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQKLVFF 8
          ||:||||
Db      1 HQELVFF 7


RESULT 24
AAR87921
ID   AAR87921 standard; peptide; 7 AA.
XX
AC   AAR87921;
XX
DT   01-MAR-1996  (first entry)
XX
DE   Test peptide used in study of antagonism of amyloid beta protein.
XX
KW   amnesia; amyloid beta; Alzheimer's disease.
XX
OS   Synthetic.
XX
PN   WO9508999-A1.
XX
PD   06-APR-1995.
XX
```

```
PF   16-SEP-1994;   94WO-US10475.
XX
PR   29-SEP-1993;   93US-0127904.
XX
PA   (CITY ) CITY OF HOPE.
XX
PI   Roberts E;
XX
DR   WPI; 1995-147244/19.
XX
PT   New peptide(s) which block binding of amyloid beta protein - used
PT   for antagonising the amnestic effects of amyloid beta protein,
PT   partic. in Alzheimer's disease
XX
PS   Disclosure; Page 9; 27pp; English.
XX
CC   The invention relates to three new peptides which block the amnestic
CC   effects of amyloid beta protein and which can be used to ameliorate
CC   amnesia and other neurotoxicity in Alzheimer's disease caused by
CC   deposition of this protein. The peptides themselves are not amnestic or
CC   memory-enhancing. The new peptides are described in AAR87912, AAR87913
CC   and AAR87914.
CC   The present sequence is an additional peptide tested in the process
CC   but found not to be active.
XX
SQ   Sequence   7 AA;

  Query Match             61.8%;  Score 34;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          |||||||
Db      1 KLVFFAE 7


RESULT 25
AAR88300
ID   AAR88300 standard; peptide; 7 AA.
XX
AC   AAR88300;
XX
DT   23-FEB-1996  (first entry)
XX
DE   Non-amnestic peptide Beta-A4 (16-22).
XX
KW   memory; enhancer; topographic model; amnestic peptide binding site;
KW   beta-A4.
XX
OS   Synthetic.
XX
PN   WO9507093-A1.
XX
PD   16-MAR-1995.
XX
PF   08-SEP-1994;   94WO-US10083.
XX
PR   08-SEP-1993;   93US-0117927.
XX
PA   (CITY ) CITY OF HOPE.
XX
PI   Roberts E;
XX
DR   WPI; 1995-123235/16.
XX
PT   Topographic model for amnestic peptide binding  - used to design
PT   cpds. which enhance memory; and new peptide(s) so designed
XX
PS   Disclosure; Page 28; 51pp; English.
XX
CC   The peptide AAR88300 corresponds to residues 16-22 of beta-A4 was
CC   designed as a potential memory enhancing peptide but was found not
CC   to be amnestic. (Amnestic peptides are memory-enhancing at lower
CC   concentrations than those at which they cause amnesia).
XX
SQ   Sequence   7 AA;

  Query Match             61.8%;  Score 34;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          |||||||
Db      1 KLVFFAE 7


RESULT 26
AAR80370
ID   AAR80370 standard; peptide; 7 AA.
XX
AC   AAR80370;
XX
DT   19-APR-1996  (first entry)
XX
DE   Protein polymeric adhesion substrate glutamine donor peptide #20.
XX
KW   Pendent group; repeating unit; enzyme recognition site; sealant; fibrin;
KW   enzymatic cross-linking; biocompatible material; structural integrity;
KW   medical adhesive; wound closure; tissue repair; transglutaminase;
KW   protein polymer adhesive substrate.
XX
OS   Synthetic.
XX
PN   WO9523611-A1.
XX
PD   08-SEP-1995.
XX
PF   03-MAR-1995;   95WO-US02728.
XX
PR   03-MAR-1994;   94US-0205518.
XX
PA   (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI   Cappello J;
XX
DR   WPI; 1995-320413/41.
XX
PT   Protein polymers comprising repeating units and sequences  - capable
PT   of enzyme-catalysed covalent bond formation useful as a
PT   biocompatible material for wound closure and tissue repair
XX
PS   Example 9; Page 75; 138pp; English.
XX
CC   The peptides AAR80351-70 are examples of glutamine donor peptides which
CC   can be used to generate protein polymeric adhesion substrate (PPAS)
CC   contg. repeats of non-fibrin cross-linking donor peptide sequences (see
CC   AAR80345-50 for examples of PPAS proteins).  The PPAS proteins can be
CC   used as substrates in enzymatic cross-linking reactions catalysed by a
CC   transglutaminase enzyme e.g. Factor VIII or XIII.  The polymers can be
CC   used in biological systems where in situ formation of a biocompatible
CC   material with structural integrity is required e.g. as medical adhesives
CC   and sealants or for wound closure or tissue repair.
XX
SQ   Sequence   7 AA;

  Query Match             61.8%;  Score 34;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLV 6
          ||||||
Db      2 HHQKLV 7


RESULT 27
AAW02312
```

ID AAW02312 standard; peptide; 7 AA.
XX
AC AAW02312;
XX
DT 02-MAY-1997 (first entry)
XX
DE Beta-amyloid modulator peptide #3.
XX
KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9628471-A1.
XX
PD 19-SEP-1996.
XX
PF 14-MAR-1996; 96WO-US03492.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
XX
PA (PHAR-) PHARM PEPTIDES INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
XX
DR WPI; 1996-433762/43.
XX
PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
PT protein coupled (in)directly to at least 1 modifying gp., useful in
PT treatment of Alzheimer's disease
XX
PS Claim 16; Page 91; 106pp; English.
XX
CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
CC modulator compounds of the invention. Beta-amyloid peptide is a 4
CC kilodalton peptide that is the major protein component of amyloid
CC plaques. Amyloid plaques are present both in the brain lesions, and in
CC the walls of cerebral blood vessels in Alzheimer's disease patients.
CC The amyloid modulators of the invention comprise an amyloidogenic protein
CC or peptide (such as this sequence) coupled directly or indirectly to at
CC least one modifying group. The modifying group is preferably a cyclic,
CC heterocyclic, or polycyclic group, such as declain, a cholanyl group, a
CC biotin containing group, or a fluorescein containing group. These
CC compounds then modulate the aggregation of these sequences to natural
CC amyloid proteins or peptides when contacted with the natural
CC amyloidogenic proteins or peptides. The modulator compounds can be used
CC in the treatment of disorders associated with amyloidosis, such as
CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
CC and other types of amyloidosis. The modulators are also useful for the
CC treatment of disorders associated with beta-amyloidosis, especially
CC Alzheimer's disease.
XX
SQ Sequence 7 AA;

Query Match 61.8%; Score 34; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKLVFFA 9
|||||||
Db 1 QKLVFFA 7

RESULT 28
AAW45942
ID AAW45942 standard; peptide; 7 AA.
XX
AC AAW45942;
XX
DT 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 7 AA;

Query Match 61.8%; Score 34; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLV 6
||||||
Db 2 HHQKLV 7

RESULT 29
AAW49755
ID AAW49755 standard; Peptide; 7 AA.
XX
AC AAW49755;
XX
DT 12-OCT-1998 (first entry)
XX

DE Glutamine donor peptide.
XX
KW Protein polymer; adhesive sealant; wound healing; cross-linking.
XX
OS Synthetic.
XX
PN US5773577-A.
XX
PD 30-JUN-1998.
XX
PF 03-MAR-1994; 94US-0205518.
XX
PR 02-MAR-1995; 95US-0397633.
PR 03-MAR-1994; 94US-0205518.
XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Cappello J;
XX
DR WPI; 1998-387091/33.
XX
PT New recombinant protein polymers - containing naturally occurring
PT repetitive units for crosslinking by enzymes, useful as medical
PT adhesives and sealants, depots and matrices
XX
PS Example 9; Column 49; 70pp; English.
XX
CC This is an example of a glutamine donor peptide that can be
CC utilised in novel recombinant protein polymers of the invention.
CC Such polymers (see AAW49710-28) typically comprise a repetitive
CC amino acid backbone of repetitive units having a collagen, fibroin,
CC elastin or keratin motif and at least 2 enzyme recognition
CC sequences comprising a glutamine and/or lysine capable of enzyme
CC catalysed isopeptide formation. The polymers are capable of
CC covalent crosslinking by enzymatic reaction to form products which
CC set quickly and have good adhesive properties and high strength.
CC They can be used as medical adhesives and sealants, in the closure
CC of wounds and repair of damaged tissues, prosthesis coatings, drug
CC depots, and matrices for the transplantation of cells.
XX
SQ Sequence 7 AA;

Query Match 61.8%; Score 34; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLV 6
||||||
Db 2 HHQKLV 7

RESULT 30
AAW89376
ID AAW89376 standard; peptide; 7 AA.
XX
AC AAW89376;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-15-21.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Example 12; Column 64; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 7 AA;

Query Match 61.8%; Score 34; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKLVFFA 9
|||||||
Db 1 QKLVFFA 7

RESULT 31
AAB67281
ID AAB67281 standard; peptide; 7 AA.
XX
AC AAB67281;
XX
DT 20-APR-2001 (first entry)
XX
DE Residues 16-22 of Alzheimer's Abeta peptide.
XX
KW Alzheimer's; Abeta; beta-strand.
XX
OS Homo sapiens.
XX
PN WO200107473-A1.
XX
PD 01-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-GB02901.
XX
PR 28-JUL-1999; 99GB-0017724.
XX
PA (STOT/) STOTT K.
XX
PI Stott K;
XX
DR WPI; 2001-182777/18.
XX
PT Novel chemical compound or composition useful for preventing

PT beta-strand association, comprises peptides containing N-alpha
PT substituted L-amino acids -
XX
PS Claim 17; Page 46; 77pp; English.
XX
CC The present invention relates to a chemical compound or composition
CC comprising a peptide with a beta strand forming section and
CC associates with a target beta-strand formed by a separate
CC peptide-containing molecule. The invention is useful for
CC inhibiting or reversing the association of target beta-strand,
CC formed by Alzheimer's Abeta peptide into a beta-sheet or beta-fibre
CC and the aggregation of proteins or peptides.
XX
SQ Sequence 7 AA;

Query Match 61.8%; Score 34; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KLVFFAE 10
|||||||
Db 1 KLVFFAE 7

RESULT 32
AAW45939
ID AAW45939 standard; peptide; 8 AA.
XX
AC AAW45939;
XX
DT 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 8 AA;

Query Match 61.8%; Score 34; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLV 6
||||||
Db 3 HHQKLV 8

RESULT 33
AAW32551
ID AAW32551 standard; peptide; 8 AA.
XX
AC AAW32551;
XX
DT 21-JAN-1998 (first entry)
XX
DE Amyloidogenic sequence amyloid beta-peptide.
XX
KW Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;
KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
KW Gerstmann-Straussler-Scheinker Syndrome; animal prion disease;
KW prion associated human neurodegenerative disease; scrapie;
KW spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease; mule; deer; elk; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9639834-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10220.
XX
PR 10-APR-1996; 96US-0630645.
PR 07-JUN-1995; 95US-0478326.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Baumann MH, Frangione B, Soto-Jara C;
XX
DR WPI; 1997-051637/05.
XX
PT New inhibitors of fibrillogenesis proteins or peptides - used for
PT preventing, treating or detecting amyloidosis disorders such as
PT Alzheimer's disease.
XX
PS Disclosure; Fig 1A; 63pp; English.
XX
CC A method has been developed for the prevention or treatment of a
CC disorder or disease associated with the formation of amyloid or
CC amyloid-like deposits, involving the abnormal folding of a protein
CC or peptide. The method involves administering an inhibitory peptide
CC which prevents the abnormal folding or which dissolves existing amyloid
CC or amyloid-like deposits, where the peptide comprises a sequence of
CC 3-15 amino acid residues and has a hydrophobic cluster of at least 3
CC amino acids, where at least one of the 3 amino acids is a beta-sheet
CC blocking amino acid residue selected from Pro, Gly, Asn and His. The
CC present sequence represents an amyloidogenic sequence, amyloid beta-
CC peptide, which is involved in the formation of several amyloid deposits.
CC The inhibitory peptide is capable of associating with a structural
CC determinant on the protein or peptide to structurally block and inhibit
CC the abnormal folding into amyloid or amyloid-like deposits. The method
CC can be used for preventing, treating or detecting e.g. Alzheimer's
CC dementia or disease, Down's syndrome, other amyloidosis disorders,
CC human prion diseases such as Kuru, Creutzfeldt-Jakob disease, Gerstmann-
CC Straussler-Scheinker Syndrome, prion associated human neurodegenerative

```
CC   diseases or animal prion diseases such as scrapie, spongiform
CC   encephalopathy, transmissible mink encephalopathy and chronic wasting
CC   disease of mule deer and elk.
XX
SQ   Sequence   8 AA;

  Query Match             61.8%;  Score 34;  DB 18;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          |||||||
Db      1 KLVFFAE 7


RESULT 34
AAE10663
ID   AAE10663 standard; peptide; 8 AA.
XX
AC   AAE10663;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX
KW   Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;
KW   Alzheimer's disease; AD; dementia;  neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   alpha-secretase.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   4..5
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-0023315.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99US-0404133.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with
PT   amyloid precursor protein processing activity and alpha-secretase
PT   activity, for identifying modulators useful in treating Alzheimer's
PT   disease -
XX
PS   Claim 10; Page 163; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC   Aspl proteins which lack transmembrane domain or amino terminal
CC   domain or cytoplasmic domain and retains alpha-secretase activity
CC   and amyloid protein precursor (APP) processing activity. The proteins
CC   of the invention are useful for assaying hu-Aspl alpha-secretase
CC   activity, which in turn is useful for identifying modulators of
CC   hu-Aspl alpha-secretase activity, where modulators that increase
CC   hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC   disease (AD) which causes progressive dementia with consequent
CC   formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC   neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC   hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC   the substrate under acidic conditions and determining the level of
CC   hu-Aspl proteolytic activity. The present sequence is human amyloid
CC   precursor protein (APP) substrate alpha-secretase peptide which is
CC   used for determining the enzymatic activity of Asp-1 protein lacking
CC   transmembrane domain (TM) and containing a (His)6 tag.
XX
SQ   Sequence   8 AA;

  Query Match             61.8%;  Score 34;  DB 22;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          |||||||
Db      1 KLVFFAE 7


RESULT 35
AAE02615
ID   AAE02615 standard; peptide; 8 AA.
XX
AC   AAE02615;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
KW   beta-secretase.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   4..5
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26080.
XX
PR   23-SEP-1999;   99US-0155493.
PR   23-SEP-1999;   99WO-US20881.
PR   13-OCT-1999;   99US-0416901.
PR   06-DEC-1999;   99US-0169232.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M,  Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Claim 10; Page 98; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human amyloid precursor
CC   protein (APP) substrate alpha-secretase peptide which is used for
CC   determining the enzymatic activity of Asp-1 deltaTM (His)6 protein.
XX
SQ   Sequence   8 AA;

  Query Match             61.8%;  Score 34;  DB 22;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
```

```
              |||||||
Db       1 KLVFFAE 7


RESULT 36
AAY79938
ID   AAY79938 standard; peptide; 10 AA.
XX
AC   AAY79938;
XX
DT   11-MAY-2000  (first entry)
XX
DE   Beta-amyloid recognition peptide SEQ ID NO:3.
XX
KW   Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;
KW   Alzheimer's disease; neuroprotective; nootropic.
XX
OS   Homo sapiens.
XX
PN   US6022859-A.
XX
PD   08-FEB-2000.
XX
PF   14-NOV-1997;   97US-0970833.
XX
PR   15-NOV-1996;   96US-0030840.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Murphy RM,  Kiessling LL;
XX
DR   WPI; 2000-160387/14.
XX
PT   Beta-amyloid inhibitor useful for treating Alzheimer's disease -
XX
PS   Example; Column 7; 15pp; English.
XX
CC   The present invention describes a beta-amyloid inhibitor peptide.
CC   Beta-amyloid inhibitors have neuroprotective and nootropic
CC   properties. The inhibitor peptides are useful for the treatment of
CC   Alzheimer's disease. The present sequence represents a beta-amyloid
CC   recognition peptide used in the exemplification of present invention.
XX
SQ   Sequence   10 AA;

  Query Match             61.8%;  Score 34;  DB 21;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFFAE 10
           |||||||
Db       1 KLVFFAE 7


RESULT 37
AAB46221
ID   AAB46221 standard; peptide; 10 AA.
XX
AC   AAB46221;
XX
DT   04-APR-2001  (first entry)
XX
DE   Human APP derived immunogenic peptide #17.
XX
KW   Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW   Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW   amyloid precursor protein; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200072880-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14810.
XX
PR   28-MAY-1999;   99US-0322289.
XX
PA   (NEUR-) NEURALAB LTD.
XX
PI   Schenk DB,  Bard F,  Vasquez NJ,  Yednock T;
XX
DR   WPI; 2001-032104/04.
XX
PT   Preventing or treating a disease associated with amyloid deposits,
PT   especially Alzheimer's disease, comprises administering amyloid
PT   specific antibody  -
XX
PS   Disclosure; Figure 19; 143pp; English.
XX
CC   This invention describes a novel method of preventing or treating a
CC   disease associated with amyloid deposits of amyloid precursor protein
CC   (APP) Abeta fragments in the brain of a patient, which comprises
CC   administering to the patient: (a) an antibody that binds to Abeta, the
CC   antibody binds to an amyloid deposit and induces a clearing response (Fc
CC   receptor mediated phagocytosis) against it (b) a polypeptide containing
CC   an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC   that induces an immunogenic response against residues 1-3 to 7-11 of
CC   Abeta. The products of the invention have nootropic and neuroprotective
CC   activity. The method is also useful for monitoring a course of treatment
CC   being administered to a patient e.g. active and passive immunization. The
CC   methods are useful for prophylactic and therapeutic treatment of
CC   Alzheimer's disease.
XX
SQ   Sequence   10 AA;

  Query Match             61.8%;  Score 34;  DB 22;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||||
Db       5 HHQKLV 10


RESULT 38
AAB46228
ID   AAB46228 standard; peptide; 10 AA.
XX
AC   AAB46228;
XX
DT   04-APR-2001  (first entry)
XX
DE   Human APP derived immunogenic peptide #24.
XX
KW   Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW   Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW   amyloid precursor protein; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200072880-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14810.
XX
PR   28-MAY-1999;   99US-0322289.
XX
PA   (NEUR-) NEURALAB LTD.
XX
PI   Schenk DB,  Bard F,  Vasquez NJ,  Yednock T;
XX
DR   WPI; 2001-032104/04.
XX
PT   Preventing or treating a disease associated with amyloid deposits,
```

PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 61.8%; Score 34; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KLVFFAE 10
|||||||
Db 1 KLVFFAE 7

RESULT 39
AAW45945
ID AAW45945 standard; peptide; 6 AA.
XX
AC AAW45945;
XX
DT 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 6 AA;

Query Match 58.2%; Score 32; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVF 7
||||||
Db 1 HQKLVF 6

RESULT 40
AAR45233
ID AAR45233 standard; Peptide; 7 AA.
XX
AC AAR45233;
XX
DT 20-JUN-1994 (first entry)
XX
DE Beta amyloid protein fragment.
XX
KW Amyloid precursor protein; APP; beta amyloid protein; BAP;
KW detection; Alzheimer's disease; Down's syndrome.
XX
OS Homo sapiens.
XX
PN AU9338358-A.
XX
PD 04-NOV-1993.
XX
PF 03-MAY-1993; 93AU-0038358.
XX
PR 01-MAY-1992; 92US-0877675.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR WPI; 1993-406194/51.
DR N-PSDB; AAQ54261.
XX
PT New mutant forms of amyloid precursor protein - for detecting
PT cpds. that modify activity of enzymes involved in precursor
PT cleavage, also new nucleic acid encoding them
XX
PS Disclosure; Page 34; 66pp; English.
XX
CC Recombinant polypeptides produced using the coding sequences of
CC mutant forms of amyloid precursor proteins comprising from the 5' to
CC the 3' end a sequence encoding a marker and either (1) a sequence
CC encoding the N-terminus of an amyloid precursor protein (APP) up to,
CC but not including, the nucleotides encoding the beta amyloid protein
CC (BAP) domain or (2) the BAP domain; or the two ligated together, can
CC be used to detect drugs or compounds that inhibit/augment the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments (deposition of which occurs in patients with Alzheimers
CC disease and Down's syndrome). This fragment corresponding to amino
CC acid residues 14-20 of BAP has been altered and APP's containing
CC the altered BAP sequence show 10-20% secretion compared with those
CC containing the wild type BAP sequence.
XX
SQ Sequence 7 AA;

Query Match 56.4%; Score 31; DB 14; Length 7;
Best Local Similarity 85.7%; Pred. No. 6.4e+05;

```
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 HQKLVFF 8
           || ||||
Db       1 HQVLVFF 7


RESULT 41
AAB82639
ID   AAB82639 standard; Peptide; 7 AA.
XX
AC   AAB82639;
XX
DT   02-OCT-2001  (first entry)
XX
DE   All-D peptide used in Alzheimer's disease vaccine.
XX
KW   Alzheimer's disease; amyloidosis; amyloid-related disease;
KW   vaccine; therapy; antigen.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..7
FT                   /note= "all D-form residues"
XX
PN   WO200139796-A2.
XX
PD   07-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-CA01413.
XX
PR   29-NOV-1999;   99US-0168594.
PR   28-NOV-2000; 2000US-0724842.
XX
PA   (NEUR-) NEUROCHEM INC.
XX
PI   Chalifour R,  Hebert L,  Kong X,  Gervais F;
XX
DR   WPI; 2001-441458/47.
XX
PT   Preventing/treating amyloid-related disease, especially Alzheimer's
PT   disease, comprises administering antigenic all-D peptide, e.g. as
PT   vaccine, which elicits production of antibodies to prevent
PT   fibrillogenesis and associated cellular toxicity -
XX
PS   Disclosure; Page 11; 31pp; English.
XX
CC   The present sequence is that of an all-D peptide suitable for
CC   use in preparing vaccines for preventing or treating Alzheimer's
CC   disease and other amyloid related disorders in humans.  It is based
CC   on a portion of amyloid-beta peptide (see AAB82622), and may be
CC   modified by removing or inserting 1 or more amino acid residues, or
CC   by substituting 1 or more amino acid residues with other amino acid
CC   residues or non-amino acid fragments.  Vaccines of the invention
CC   are produced using 'non-self' peptides synthesised from the
CC   unnatural D-configuration amino acids to avoid the drawbacks of
CC   'self' proteins.  The all-D peptides need not be aggregated to be
CC   operative or immunogenic.  They preferably interact with at
CC   least 1 region of an amyloid protein, e.g. the beta-sheet region
CC   or GAG-binding site region, the amyloid-beta peptide, or their
CC   immunogenic fragments, protein conjugates, immunogenic derivative
CC   peptides and immunogenic peptidomimetics.  Examples include all-D
CC   peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
CC   10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
CC   derivative peptides given in AAB82623-64.  The vaccine elicits a
CC   preferential TH-2 or TH-1 response, preventing fibrillogenesis and
CC   associated cellular toxicity.  The amyloid related diseases may be
CC   localised amyloidosis, e.g. diabetes type II, neurodegenerative
CC   diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
CC   disease, scrapie, cerebral amyloid angiopathy, and prion protein
CC   related disorders, or systemic amyloidosis associated with chronic
CC   infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC   rheumatoid arthritis), familial Mediterranean fever (FMF) and
CC   systemic amyloidosis found in long-term haemodialysis patients.
XX
SQ   Sequence   7 AA;

  Query Match             56.4%;  Score 31;  DB 22;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFFAE 10
           ||||||:
Db       1 KLVFFAQ 7


RESULT 42
AAB82640
ID   AAB82640 standard; Peptide; 7 AA.
XX
AC   AAB82640;
XX
DT   02-OCT-2001  (first entry)
XX
DE   All-D peptide used in Alzheimer's disease vaccine.
XX
KW   Alzheimer's disease; amyloidosis; amyloid-related disease;
KW   vaccine; therapy; antigen.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..7
FT                   /note= "all D-form residues"
FT   Modified-site   6
FT                   /note= "C-terminal amide"
XX
PN   WO200139796-A2.
XX
PD   07-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-CA01413.
XX
PR   29-NOV-1999;   99US-0168594.
PR   28-NOV-2000; 2000US-0724842.
XX
PA   (NEUR-) NEUROCHEM INC.
XX
PI   Chalifour R,  Hebert L,  Kong X,  Gervais F;
XX
DR   WPI; 2001-441458/47.
XX
PT   Preventing/treating amyloid-related disease, especially Alzheimer's
PT   disease, comprises administering antigenic all-D peptide, e.g. as
PT   vaccine, which elicits production of antibodies to prevent
PT   fibrillogenesis and associated cellular toxicity -
XX
PS   Disclosure; Page 11; 31pp; English.
XX
CC   The present sequence is that of an all-D peptide suitable for
CC   use in preparing vaccines for preventing or treating Alzheimer's
CC   disease and other amyloid related disorders in humans.  It is based
CC   on a portion of amyloid-beta peptide (see AAB82622), and may be
CC   modified by removing or inserting 1 or more amino acid residues, or
CC   by substituting 1 or more amino acid residues with other amino acid
CC   residues or non-amino acid fragments.  Vaccines of the invention
CC   are produced using 'non-self' peptides synthesised from the
CC   unnatural D-configuration amino acids to avoid the drawbacks of
CC   'self' proteins.  The all-D peptides need not be aggregated to be
CC   operative or immunogenic.  They preferably interact with at
CC   least 1 region of an amyloid protein, e.g. the beta-sheet region
CC   or GAG-binding site region, the amyloid-beta peptide, or their
CC   immunogenic fragments, protein conjugates, immunogenic derivative
CC   peptides and immunogenic peptidomimetics.  Examples include all-D
CC   peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
```

```
CC   10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
CC   derivative peptides given in AAB82623-64.  The vaccine elicits a
CC   preferential TH-2 or TH-1 response, preventing fibrillogenesis and
CC   associated cellular toxicity.  The amyloid related diseases may be
CC   localised amyloidosis, e.g. diabetes type II, neurodegenerative
CC   diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
CC   disease, scrapie, cerebral amyloid angiopathy, and prion protein
CC   related disorders, or systemic amyloidosis associated with chronic
CC   infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC   rheumatoid arthritis), familial Mediterranean fever (FMF) and
CC   systemic amyloidosis found in long-term haemodialysis patients.
XX
SQ   Sequence   7 AA;

  Query Match             56.4%;  Score 31;  DB 22;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          ||||||:
Db      1 KLVFFAQ 7


RESULT 43
AAB48491
ID   AAB48491 standard; Peptide; 7 AA.
XX
AC   AAB48491;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Antifibrillogenic peptide #18.
XX
KW   Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW   cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200068263-A2.
XX
PD   16-NOV-2000.
XX
PF   04-MAY-2000; 2000WO-CA00515.
XX
PR   05-MAY-1999;   99US-0132592.
XX
PA   (NEUR-) NEUROCHEM INC.
XX
PI   Chalifour R,  Gervais F,  Gupta A;
XX
DR   WPI; 2001-031852/04.
XX
PT   Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT   cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT   its isomer or peptidomimetic -
XX
PS   Claim 7; Page 25; 46pp; English.
XX
CC   Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC   for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC   AAB48474-B48496 cause the breakdown of amyloid deposits and are
CC   therefore useful for treating amyloidosis disorders such as Alzheimer's
CC   disease. Peptides AAB48474-B48496 were identified from the
CC   glycosaminoglycan binding region and the prot-prot interaction region of
CC   the human amyloid protein.
XX
SQ   Sequence   7 AA;

  Query Match             56.4%;  Score 31;  DB 22;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          ||||||:
Db      1 KLVFFAQ 7


RESULT 44
AAB48492
ID   AAB48492 standard; Peptide; 7 AA.
XX
AC   AAB48492;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Antifibrillogenic peptide #19.
XX
KW   Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW   cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "C-terminal amide"
XX
PN   WO200068263-A2.
XX
PD   16-NOV-2000.
XX
PF   04-MAY-2000; 2000WO-CA00515.
XX
PR   05-MAY-1999;   99US-0132592.
XX
PA   (NEUR-) NEUROCHEM INC.
XX
PI   Chalifour R,  Gervais F,  Gupta A;
XX
DR   WPI; 2001-031852/04.
XX
PT   Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT   cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT   its isomer or peptidomimetic -
XX
PS   Claim 7; Page 25; 46pp; English.
XX
CC   Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC   for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC   AAB48474-B48496 cause the breakdown of amyloid deposits and are
CC   therefore useful for treating amyloidosis disorders such as Alzheimer's
CC   disease. Peptides AAB48474-B48496 were identified from the
CC   glycosaminoglycan binding region and the prot-prot interaction region of
CC   the human amyloid protein.
XX
SQ   Sequence   7 AA;

  Query Match             56.4%;  Score 31;  DB 22;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          ||||||:
Db      1 KLVFFAQ 7


RESULT 45
AAW45952
ID   AAW45952 standard; peptide; 5 AA.
XX
AC   AAW45952;
XX
DT   30-JUN-1998  (first entry)
XX
DE   Amyloid beta peptide fragment.
```

XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 5 AA;

Query Match 54.5%; Score 30; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKL 5
|||||
Db 1 HHQKL 5

RESULT 46
AAW02313
ID AAW02313 standard; peptide; 6 AA.
XX
AC AAW02313;
XX
DT 02-MAY-1997 (first entry)
XX
DE Beta-amyloid modulator peptide #4.
XX
KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9628471-A1.
XX
PD 19-SEP-1996.
XX
PF 14-MAR-1996; 96WO-US03492.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
XX
PA (PHAR-) PHARM PEPTIDES INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
XX
DR WPI; 1996-433762/43.
XX
PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
PT protein coupled (in)directly to at least 1 modifying gp., useful in
PT treatment of Alzheimer's disease
XX
PS Claim 16; Page 91; 106pp; English.
XX
CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
CC modulator compounds of the invention. Beta-amyloid peptide is a 4
CC kilodalton peptide that is the major protein component of amyloid
CC plaques. Amyloid plaques are present both in the brain lesions, and in
CC the walls of cerebral blood vessels in Alzheimer's disease patients.
CC The amyloid modulators of the invention comprise an amyloidogenic protein
CC or peptide (such as this sequence) coupled directly or indirectly to at
CC least one modifying group. The modifying group is preferably a cyclic,
CC heterocyclic, or polycyclic group, such as declain, a cholanyl group, a
CC biotin containing group, or a fluorescein containing group. These
CC compounds then modulate the aggregation of these sequences to natural
CC amyloid proteins or peptides when contacted with the natural
CC amyloidogenic proteins or peptides. The modulator compounds can be used
CC in the treatment of disorders associated with amyloidosis, such as
CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
CC and other types of amyloidosis. The modulators are also useful for the
CC treatment of disorders associated with beta-amyloidosis, especially
CC Alzheimer's disease.
XX
SQ Sequence 6 AA;

Query Match 54.5%; Score 30; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKLVFF 8
||||||
Db 1 QKLVFF 6

RESULT 47
AAW45947
ID AAW45947 standard; peptide; 6 AA.
XX
AC AAW45947;
XX
DT 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX

PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 6 AA;

Query Match 54.5%; Score 30; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKL 5
|||||
Db 2 HHQKL 6

RESULT 48
AAW45944
ID AAW45944 standard; peptide; 6 AA.
XX
AC AAW45944;
XX
DT 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9721728-A1.
XX
PD 19-JUN-1997.
XX
PF 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 6 AA;

Query Match 54.5%; Score 30; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKL 5
|||||
Db 2 HHQKL 6

RESULT 49
AAY39801
ID AAY39801 standard; peptide; 6 AA.
XX
AC AAY39801;
XX
DT 29-NOV-1999 (first entry)
XX
DE Beta-amyloid protein fragment.
XX
KW Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
KW long-standing inflammation; malignancy; Familial Mediterranean Fever;
KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
KW Creutzfeldt-Jakob disease; Gerstmann Strausiler Syndrome;
KW subacute spongiform encephalopathy; therapy.
XX
OS Homo sapiens.
XX
PN US5958883-A.
XX
PD 28-SEP-1999.
XX
PF 05-JUN-1995; 95US-0461216.
XX
PR 23-OCT-1992; 92US-0969734.
PR 23-SEP-1992; 92US-0950417.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Snow AD;
XX
DR WPI; 1999-561062/47.
XX
PT Peptides of 6-8 amino acids useful for treating or preventing
PT amyloidosis -

XX
PS Claim 1; Column 71; 83pp; English.
XX
CC This sequence represents a fragment of the beta-amyloid protein. The
CC invention relates to a method for treating or preventing a form of
CC amyloidosis, including Alzheimer's disease using this sequence. The
CC compositions may be useful for treating or preventing the amyloidosis
CC associated with long-standing inflammation, various forms of malignancy
CC (including B-cell type malignancies), Familial Mediterranean Fever,
CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
CC Creutzfeldt-Jakob disease, Gerstmann Strausiler Syndrome, kuru, scrapie
CC and other subacute spongiform encephalopathies.
XX
SQ Sequence 6 AA;

Query Match 54.5%; Score 30; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKL 5
|||||
Db 2 HHQKL 6

RESULT 50
AAW29090
ID AAW29090 standard; peptide; 6 AA.
XX
AC AAW29090;
XX
DT 20-JUL-1999 (first entry)
XX
DE A-beta-binding peptide fragment conjugated to cyclosporin.
XX
KW Cyclosporin; A-beta peptide; conjugate; neurological disease;
KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;
KW ALS; non-immunosuppressive; amyloid plaque formation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "The C-terminal is condensed onto the side
FT chain of Lys(7) of the cyclosporin analog described
FT in AAW29087, AAW29088, AAW29095 and AAW29097"
XX
PN WO9910374-A1.
XX
PD 04-MAR-1999.
XX
PF 25-AUG-1998; 98WO-US17544.
XX
PR 26-AUG-1997; 97US-0057751.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Rich DH, Solomon ME;
XX
DR WPI; 1999-276928/23.
XX
PT New A-beta-binding peptide conjugates and CsA analogs - useful in
PT treatment of neurological diseases e.g. Alzheimer's disease,
PT multiple sclerosis etc.
XX
PS Claim 5; Page 98; 129pp; English.
XX
CC New conjugates are disclosed which are of formula A-Z, in which: A is
CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506
CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more
CC contiguous residues of A-beta peptide. The compounds are novel chemical
CC inducers of dimerization which are non-immunosuppressive and which are
CC inhibitors of A-beta peptide aggregation and deposition in amyloid
CC plaques. The adverse consequences of amyloid plaque formation can be
CC prevented or ameliorated by sequestering the A-beta peptide in monomeric
CC form with a conjugate which links the A-beta to cyclophilin or FKBP,
CC therefore providing a mechanism to minimize the amount of free A-beta
CC available for fibril formation and deposition. The compounds can be used
CC for the treatment of Alzheimer's disease, multiple sclerosis and
CC amyotrophic lateral sclerosis.
XX
SQ Sequence 6 AA;

Query Match 54.5%; Score 30; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKLVFF 8
||||||
Db 1 QKLVFF 6

Search completed: October 29, 2002, 09:37:39
Job time : 31 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:27 ; Search time 13 Seconds
(without alignments)
18.789 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	15	2	US-08-612-785B-37	Sequence 37, Appl
2	55	100.0	17	4	US-09-264-709A-2	Sequence 2, Appli
3	55	100.0	26	1	US-08-304-585-7	Sequence 7, Appli
4	55	100.0	28	1	US-08-346-849-4	Sequence 4, Appli
5	55	100.0	28	1	US-08-302-808-7	Sequence 7, Appli
6	55	100.0	28	2	US-08-609-090-2	Sequence 2, Appli
7	55	100.0	28	2	US-08-986-948-7	Sequence 7, Appli
8	55	100.0	28	2	US-08-293-284A-4	Sequence 4, Appli
9	55	100.0	28	2	US-08-461-216-2	Sequence 2, Appli
10	55	100.0	28	4	US-09-388-890-2	Sequence 2, Appli
11	55	100.0	28	4	US-09-388-890-3	Sequence 3, Appli
12	55	100.0	28	4	US-09-388-890-4	Sequence 4, Appli
13	55	100.0	28	4	US-09-388-890-5	Sequence 5, Appli
14	55	100.0	28	4	US-09-388-890-6	Sequence 6, Appli
15	55	100.0	28	4	US-09-388-890-7	Sequence 7, Appli
16	55	100.0	28	4	US-09-388-890-8	Sequence 8, Appli
17	55	100.0	28	4	US-09-388-890-13	Sequence 13, Appl
18	55	100.0	28	4	US-09-388-890-14	Sequence 14, Appl
19	55	100.0	28	4	US-09-264-709A-1	Sequence 1, Appli
20	55	100.0	28	4	US-08-723-661B-2	Sequence 2, Appli
21	55	100.0	30	2	US-08-609-090-3	Sequence 3, Appli
22	55	100.0	33	2	US-08-609-090-4	Sequence 4, Appli
23	55	100.0	35	1	US-08-304-585-6	Sequence 6, Appli
24	55	100.0	35	2	US-08-612-785B-36	Sequence 36, Appl
25	55	100.0	35	2	US-08-612-785B-38	Sequence 38, Appl
26	55	100.0	35	2	US-08-612-785B-40	Sequence 40, Appl
27	55	100.0	36	2	US-08-609-090-6	Sequence 6, Appli
28	55	100.0	38	1	US-08-302-808-1	Sequence 1, Appli
29	55	100.0	38	2	US-07-737-371E-68	Sequence 68, Appl
30	55	100.0	38	2	US-08-986-948-1	Sequence 1, Appli
31	55	100.0	39	1	US-08-304-585-5	Sequence 5, Appli
32	55	100.0	39	1	US-08-302-808-2	Sequence 2, Appli
33	55	100.0	39	2	US-08-609-090-7	Sequence 7, Appli
34	55	100.0	39	2	US-08-682-245A-1	Sequence 1, Appli
35	55	100.0	39	2	US-08-986-948-2	Sequence 2, Appli
36	55	100.0	40	1	US-07-744-767A-1	Sequence 1, Appli
37	55	100.0	40	1	US-08-235-400-2	Sequence 2, Appli
38	55	100.0	40	1	US-08-476-464A-2	Sequence 2, Appli
39	55	100.0	40	1	US-08-304-585-1	Sequence 1, Appli
40	55	100.0	40	1	US-08-302-808-3	Sequence 3, Appli
41	55	100.0	40	2	US-08-433-734-1	Sequence 1, Appli
42	55	100.0	40	2	US-08-609-090-8	Sequence 8, Appli
43	55	100.0	40	2	US-07-737-371E-69	Sequence 69, Appl
44	55	100.0	40	2	US-08-682-245A-2	Sequence 2, Appli
45	55	100.0	40	2	US-08-986-948-3	Sequence 3, Appli
46	55	100.0	40	2	US-08-461-216-1	Sequence 1, Appli
47	55	100.0	40	4	US-08-959-148-1	Sequence 1, Appli
48	55	100.0	40	4	US-09-242-724-22	Sequence 22, Appl
49	55	100.0	40	4	US-08-723-661B-1	Sequence 1, Appli
50	55	100.0	40	5	PCT-US92-06700-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-612-785B-37

  Query Match             100.0%;  Score 55;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db      3 HHQKLVFFAE 12


RESULT 2
US-09-264-709A-2
; Sequence 2, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
;  APPLICANT:  Roberts, Eugene
;  TITLE OF INVENTION:  Method for Design of Substances that Enhance Memory and
;  TITLE OF INVENTION:  Improve the Quality of Life
;  FILE REFERENCE:  2124-310
;  CURRENT APPLICATION NUMBER: US/09/264,709A
;  CURRENT FILING DATE:  1999-03-09
;  PRIOR APPLICATION NUMBER:  08/797,782
;  PRIOR FILING DATE:  1997-02-07
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-264-709A-2

  Query Match             100.0%;  Score 55;  DB 4;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db      2 HHQKLVFFAE 11


RESULT 3
US-08-304-585-7
; Sequence 7, Application US/08304585
; Patent No. 5721106
;  GENERAL INFORMATION:
;    APPLICANT:  Maggio, John E.
;    APPLICANT:  Mantyh, Patrick W.
;    TITLE OF INVENTION:  LABELLED BETA-AMYLOID PEPTIDE AND
;    TITLE OF INVENTION:  METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  P.O. Box 581415
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55458-1415
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/304,585
;      FILING DATE:  12-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  110.00010120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1217
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-304-585-7

  Query Match             100.0%;  Score 55;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.00023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db      4 HHQKLVFFAE 13


RESULT 4
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
;  GENERAL INFORMATION:
;    APPLICANT:  Zhang, Shuguang
;    APPLICANT:  Lockshin, Curtis
;    APPLICANT:  Rich, Alexander
;    APPLICANT:  Holmes, Todd
;    TITLE OF INVENTION:  STABLE MACROSCOPIC MEMBRANES FORMED BY
;    TITLE OF INVENTION:  SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02173-4799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/346,849
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,326
;      FILING DATE:  28 DECEMBER 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  MIT-6008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-346-849-4

  Query Match             100.0%;  Score 55;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 5
US-08-302-808-7
; Sequence 7, Application US/08302808
; Patent No. 5750349
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5750349uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/302,808
;      FILING DATE:  15-SEP-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/00089
;      FILING DATE:  24-JAN-1994
;      APPLICATION NUMBER:  010132/1993
;      FILING DATE:  25-JAN-1993
;      APPLICATION NUMBER:  019035/1993
;      FILING DATE:  05-FEB-1993
;      APPLICATION NUMBER:  286985/1993
;      FILING DATE:  16-NOV-1993
;      APPLICATION NUMBER:  334773/1993
;      FILING DATE:  28-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  44631
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-302-808-7

  Query Match           100.0%;  Score 55;  DB 1;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 6
US-08-609-090-2
; Sequence 2, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,090
;      FILING DATE:  29-FEB-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kraus, Eric J.
;      REGISTRATION NUMBER:  36,190
;      REFERENCE/DOCKET NUMBER:  434-059
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-684-1111
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-609-090-2

  Query Match           100.0%;  Score 55;  DB 2;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 7
US-08-986-948-7
; Sequence 7, Application US/08986948
; Patent No. 5955317
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5955317uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
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;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/986,948
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/302,808
;       FILING DATE:  15-SEP-1994
;       APPLICATION NUMBER:  PCT/JP94/00089
;       FILING DATE:  24-JAN-1994
;       APPLICATION NUMBER:  010132/1993
;       FILING DATE:  25-JAN-1993
;       APPLICATION NUMBER:  019035/1993
;       FILING DATE:  05-FEB-1993
;       APPLICATION NUMBER:  286985/1993
;       FILING DATE:  16-NOV-1993
;       APPLICATION NUMBER:  334773/1993
;       FILING DATE:  28-DEC-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DAVID, RESNICK S
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  44631
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;       TELEX:  200291 STRE
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  28 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
US-08-986-948-7

  Query Match             100.0%;  Score 55;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 8
US-08-293-284A-4
; Sequence 4, Application US/08293284A
; Patent No. 5955343
;  GENERAL INFORMATION:
;    APPLICANT:  Holmes, Todd
;    APPLICANT:  Zhang, Shuguang
;    APPLICANT:  Rich, Alexander
;    APPLICANT:  DiPersio, C. Michael
;    APPLICANT:  Lockshin, Curtis
;    TITLE OF INVENTION:  STABLE MACROSCOPIC MEMBRANES FORMED BY
;    TITLE OF INVENTION:  SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02173-4799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/293,284A
;       FILING DATE:  22-AUG-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/973,326
;       FILING DATE:  28-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brook, David E.
;       REGISTRATION NUMBER:  22,592
;       REFERENCE/DOCKET NUMBER:  MIT-6008A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 861-6240
;       TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  28 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-293-284A-4

  Query Match             100.0%;  Score 55;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 9
US-08-461-216-2
; Sequence 2, Application US/08461216
; Patent No. 5958883
;  GENERAL INFORMATION:
;    APPLICANT:  Snow, A.D.
;    TITLE OF INVENTION:  ANIMAL MODELS OF HUMAN AMYLOIDOSES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson and Kindness
;      STREET:  1420 Fifth Avenue, Suite 2800
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette-5.25 inch, 1.2Mb storage
;      COMPUTER:  IBM PC/386 Compatible
;      OPERATING SYSTEM:  MS-DOS 4.01
;      SOFTWARE:  Word for Windows-t
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,216
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/969,734
;      FILING DATE:  October 23, 1992
;      APPLICATION NUMBER:  07/950,417
;      FILING DATE:  September 23, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Broderick, Thomas F.
;      REGISTRATION NUMBER:  31,332
;      REFERENCE/DOCKET NUMBER:  UOFW-1-6707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-206-682-8100; 1-206-224-0709 (direct)
;      TELEFAX:  1-206-224-0779
;      TELEX:  4938023
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH:  28 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;       DESCRIPTION:  {SYMBOL 98 \f "Symbol"}/A4(1-28);
;       DESCRIPTION:  page 83, line 31
US-08-461-216-2

  Query Match             100.0%;  Score 55;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 10
US-09-388-890-2
; Sequence 2, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  B(1-28) peptide of amyloid B protein
US-09-388-890-2

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 11
US-09-388-890-3
; Sequence 3, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  D1N B(1-28) peptide of amyloid B protein
US-09-388-890-3

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 12
US-09-388-890-4
; Sequence 4, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
```

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;       COUNTRY:  US
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/388,890
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/686,959
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  AUERBACH, JEFFREY I.
;       REGISTRATION NUMBER:  32,680
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 383-7451
;       TELEFAX:  (202) 383-6610
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  28 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  YES
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
;       ORGANISM:  HOMO SAPIENS
;     IMMEDIATE SOURCE:
;       CLONE:  E3Q B(1-28) peptide of amyloid B protein
US-09-388-890-4

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 13
US-09-388-890-5
; Sequence 5, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  R5Q B(1-28) peptide of amyloid B protein
US-09-388-890-5

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 14
US-09-388-890-6
; Sequence 6, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  H6Q B(1-28) peptide of amyloid B protein
```

```
US-09-388-890-6

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 15
US-09-388-890-7
; Sequence 7, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  D7Q B(1-28) peptide of amyloid B protein
US-09-388-890-7

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 16
US-09-388-890-8
; Sequence 8, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  E11Q B(1-28) peptide of amyloid B protein
US-09-388-890-8

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 17
US-09-388-890-13
; Sequence 13, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  D23Q B(1-28) peptide of amyloid B protein
US-09-388-890-13

  Query Match            100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 18
US-09-388-890-14
; Sequence 14, Application US/09388890
; Patent No. 6136548
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, STEPHEN
;    TITLE OF INVENTION:  METHODS FOR THE PREVENTION AND TREATMENT
;    TITLE OF INVENTION:  OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWREY & SIMON
;      STREET:  1299 PENNSYLVANIA AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/388,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/686,959
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I.
;      REGISTRATION NUMBER:  32,680
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 383-7451
;      TELEFAX:  (202) 383-6610
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    IMMEDIATE SOURCE:
;      CLONE:  K28Q B(1-28) peptide of amyloid B protein
US-09-388-890-14

  Query Match            100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 19
US-09-264-709A-1
; Sequence 1, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
;  APPLICANT:  Roberts, Eugene
;  TITLE OF INVENTION:  Method for Design of Substances that Enhance Memory and
;  TITLE OF INVENTION:  Improve the Quality of Life
;  FILE REFERENCE:  2124-310
;  CURRENT APPLICATION NUMBER: US/09/264,709A
;  CURRENT FILING DATE:  1999-03-09
;  PRIOR APPLICATION NUMBER:  08/797,782
;  PRIOR FILING DATE:  1997-02-07
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-264-709A-1

  Query Match            100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 20
US-08-723-661B-2
; Sequence 2, Application US/08723661B
; Patent No. 6340783
;   GENERAL INFORMATION:
;        APPLICANT: Alan D Snow
;        TITLE OF INVENTION: Animal Models of Human Amyloidoses
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Patrick M. Dwyer
;             STREET: 1818 Westlake Avenue N, Suite 114
;             CITY: Seattle
;             STATE: WA (Washington)
;             COUNTRY: United States of America
;             ZIP: 98109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
;             COMPUTER: IBM PC
;             OPERATING SYSTEM: PC-DOS (Windows 98)
;             SOFTWARE: WordPerfect 5.2
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/723,661B
;             FILING DATE: 31-Oct-1996
```

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;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/461,216
;             FILING DATE: 05-Jun-1995
;             APPLICATION NUMBER: 07/969,734
;             FILING DATE: 23-Oct-1992
;             APPLICATION NUMBER: 07/950,417
;             FILING DATE: 23-Sep-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dwyer, Patrick M.
;             REGISTRATION NUMBER: 32,411
;             REFERENCE/DOCKET NUMBER: PROTEO.P00C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 343-7074
;             TELEFAX: (206) 343-7085
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 28 AMINO ACIDS
;             TYPE: AMINO ACID
;             STRANDEDNESS: SINGLE
;             TOPOLOGY: LINEAR
;        MOLECULE TYPE: PEPTIDE
;             DESCRIPTION: /A4 (1-28); page 83, line 31
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-723-661B-2

  Query Match             100.0%;  Score 55;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 21
US-08-609-090-3
; Sequence 3, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,090
;      FILING DATE:  29-FEB-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kraus, Eric J.
;      REGISTRATION NUMBER:  36,190
;      REFERENCE/DOCKET NUMBER:  434-059
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-684-1111
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-609-090-3

  Query Match             100.0%;  Score 55;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.00027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 22
US-08-609-090-4
; Sequence 4, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,090
;      FILING DATE:  29-FEB-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kraus, Eric J.
;      REGISTRATION NUMBER:  36,190
;      REFERENCE/DOCKET NUMBER:  434-059
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-684-1111
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-609-090-4

  Query Match             100.0%;  Score 55;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.0003;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 23
US-08-304-585-6
; Sequence 6, Application US/08304585
; Patent No. 5721106
;  GENERAL INFORMATION:
;    APPLICANT:  Maggio, John E.
```

```
;    APPLICANT:  Mantyh, Patrick W.
;    TITLE OF INVENTION:  LABELLED BETA-AMYLOID PEPTIDE AND
;    TITLE OF INVENTION:  METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  P.O. Box 581415
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55458-1415
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/304,585
;      FILING DATE:  12-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  110.00010120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1217
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-304-585-6

  Query Match             100.0%;  Score 55;  DB 1;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 24
US-08-612-785B-36
; Sequence 36, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-612-785B-36

  Query Match             100.0%;  Score 55;  DB 2;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       8 HHQKLVFFAE 17


RESULT 25
US-08-612-785B-38
; Sequence 38, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  38:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-612-785B-38

  Query Match             100.0%;  Score 55;  DB 2;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 26
US-08-612-785B-40
; Sequence 40, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-612-785B-40

  Query Match             100.0%;  Score 55;  DB 2;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       8 HHQKLVFFAE 17


RESULT 27
US-08-609-090-6
; Sequence 6, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,090
;      FILING DATE:  29-FEB-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kraus, Eric J.
;      REGISTRATION NUMBER:  36,190
;      REFERENCE/DOCKET NUMBER:  434-059
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-684-1111
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-609-090-6

  Query Match             100.0%;  Score 55;  DB 2;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 28
US-08-302-808-1
; Sequence 1, Application US/08302808
; Patent No. 5750349
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5750349uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
```

```
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/302,808
;      FILING DATE:  15-SEP-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/00089
;      FILING DATE:  24-JAN-1994
;      APPLICATION NUMBER:  010132/1993
;      FILING DATE:  25-JAN-1993
;      APPLICATION NUMBER:  019035/1993
;      FILING DATE:  05-FEB-1993
;      APPLICATION NUMBER:  286985/1993
;      FILING DATE:  16-NOV-1993
;      APPLICATION NUMBER:  334773/1993
;      FILING DATE:  28-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  44631
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-302-808-1

  Query Match             100.0%;  Score 55;  DB 1;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 0.00035;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 29
US-07-737-371E-68
; Sequence 68, Application US/07737371E
; Patent No. 5876948
;  GENERAL INFORMATION:
;    APPLICANT:  Yankner, Bruce A.
;    TITLE OF INVENTION:  SCREENING METHODS TO IDENTIFY
;    TITLE OF INVENTION:  NEUROTOXIN INHIBITORS (AS AMENDED)
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/737,371E
;      FILING DATE:  29-JUL-1991
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/559,172
;      FILING DATE:  27-JUL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  00108/028002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-737-371E-68

  Query Match             100.0%;  Score 55;  DB 2;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 0.00035;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 30
US-08-986-948-1
; Sequence 1, Application US/08986948
; Patent No. 5955317
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5955317uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/986,948
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/302,808
;      FILING DATE:  15-SEP-1994
;      APPLICATION NUMBER:  PCT/JP94/00089
;      FILING DATE:  24-JAN-1994
;      APPLICATION NUMBER:  010132/1993
;      FILING DATE:  25-JAN-1993
;      APPLICATION NUMBER:  019035/1993
;      FILING DATE:  05-FEB-1993
;      APPLICATION NUMBER:  286985/1993
;      FILING DATE:  16-NOV-1993
;      APPLICATION NUMBER:  334773/1993
;      FILING DATE:  28-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
```

```
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  44631
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;       TELEX:  200291 STRE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  38 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
US-08-986-948-1

  Query Match             100.0%;  Score 55;  DB 2;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 0.00035;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 31
US-08-304-585-5
; Sequence 5, Application US/08304585
; Patent No. 5721106
;  GENERAL INFORMATION:
;    APPLICANT:  Maggio, John E.
;    APPLICANT:  Mantyh, Patrick W.
;    TITLE OF INVENTION:  LABELLED BETA-AMYLOID PEPTIDE AND
;    TITLE OF INVENTION:  METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  P.O. Box 581415
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55458-1415
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/304,585
;      FILING DATE:  12-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  110.00010120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1217
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-304-585-5

  Query Match             100.0%;  Score 55;  DB 1;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.00036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      12 HHQKLVFFAE 21


RESULT 32
US-08-302-808-2
; Sequence 2, Application US/08302808
; Patent No. 5750349
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5750349uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/302,808
;      FILING DATE:  15-SEP-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/00089
;      FILING DATE:  24-JAN-1994
;      APPLICATION NUMBER:  010132/1993
;      FILING DATE:  25-JAN-1993
;      APPLICATION NUMBER:  019035/1993
;      FILING DATE:  05-FEB-1993
;      APPLICATION NUMBER:  286985/1993
;      FILING DATE:  16-NOV-1993
;      APPLICATION NUMBER:  334773/1993
;      FILING DATE:  28-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  44631
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-302-808-2

  Query Match             100.0%;  Score 55;  DB 1;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.00036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22
```

```
RESULT 33
US-08-609-090-7
; Sequence 7, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,090
;      FILING DATE:  29-FEB-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kraus, Eric J.
;      REGISTRATION NUMBER:  36,190
;      REFERENCE/DOCKET NUMBER:  434-059
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-684-1111
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-609-090-7

  Query Match           100.0%;  Score 55;  DB 2;  Length 39;
  Best Local Similarity  100.0%;  Pred. No. 0.00036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 34
US-08-682-245A-1
; Sequence 1, Application US/08682245A
; Patent No. 5919631
;  GENERAL INFORMATION:
;    APPLICANT:  GOYAL, SHEFALI
;    APPLICANT:  PAUL, JOSEPH W
;    APPLICANT:  RIEDEL, NORBERT G
;    APPLICANT:  SAHASRABUDHE, SUDHIR
;    TITLE OF INVENTION:  A METHOD OF DETERMINING THE DEGREE OF
;    TITLE OF INVENTION:  AGGREGATION OF THE BA4 PEPTIDE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOECHST MARION ROUSSEL, INC.
;      STREET:  2110 E. GALBRAITH RD., P.O. BOX 156300
;      CITY:  CINCINNATI
;      STATE:  OHIO
;      COUNTRY:  U.S.A.
;      ZIP:  45215-6300
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/682,245A
;      FILING DATE:  17-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,414
;      FILING DATE:  16-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LENTZ, NELSEN L
;      REGISTRATION NUMBER:  38,537
;      REFERENCE/DOCKET NUMBER:  HR-1257A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  513-948-7369
;      TELEFAX:  513-948-7961 OR 4681
;      TELEX:  214320
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-682-245A-1

  Query Match           100.0%;  Score 55;  DB 2;  Length 39;
  Best Local Similarity  100.0%;  Pred. No. 0.00036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 35
US-08-986-948-2
; Sequence 2, Application US/08986948
; Patent No. 5955317
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5955317uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/986,948
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/302,808
;      FILING DATE:  15-SEP-1994
;      APPLICATION NUMBER:  PCT/JP94/00089
;      FILING DATE:  24-JAN-1994
;      APPLICATION NUMBER:  010132/1993
;      FILING DATE:  25-JAN-1993
;      APPLICATION NUMBER:  019035/1993
```

```
;      FILING DATE:  05-FEB-1993
;      APPLICATION NUMBER:  286985/1993
;      FILING DATE:  16-NOV-1993
;      APPLICATION NUMBER:  334773/1993
;      FILING DATE:  28-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  44631
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-986-948-2

  Query Match             100.0%;  Score 55;  DB 2;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.00036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 36
US-07-744-767A-1
; Sequence 1, Application US/07744767A
; Patent No. 5434050
;  GENERAL INFORMATION:
;    APPLICANT:  Maggio, John E.
;    APPLICANT:  Mantyh, Patrick W.
;    TITLE OF INVENTION:  Labelled  -Amyloid Peptide and Methods
;    TITLE OF INVENTION:  for Use in Detecting Alzheimer's Disease
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner, P.A.
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/744,767A
;      FILING DATE:  13-AUG-1991
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  600.226-US-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-744-767A-1

  Query Match             100.0%;  Score 55;  DB 1;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 37
US-08-235-400-2
; Sequence 2, Application US/08235400
; Patent No. 5552426
;  GENERAL INFORMATION:
;    APPLICANT:  Lunn, William H.
;    APPLICANT:  Monn, James A.
;    APPLICANT:  Zimmerman, Dennis M.
;    TITLE OF INVENTION:  METHODS FOR TREATING A PHYSIOLOGICAL
;    TITLE OF INVENTION:  DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center/1104
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,400
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  X-9507
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-235-400-2

  Query Match             100.0%;  Score 55;  DB 1;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 38
US-08-476-464A-2
; Sequence 2, Application US/08476464A
; Patent No. 5707821
;  GENERAL INFORMATION:
;    APPLICANT:  RYDEL, RUSSELL E.
;    APPLICANT:  DAPPEN, MICHAEL S.
;    TITLE OF INVENTION:  THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
;    TITLE OF INVENTION:  A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
```

```
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,464A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STORELLA, JOHN R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  15270-002300
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)326-2400
;      TELEFAX:  (415)576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-476-464A-2

  Query Match             100.0%;  Score 55;  DB 1;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 39
US-08-304-585-1
; Sequence 1, Application US/08304585
; Patent No. 5721106
;  GENERAL INFORMATION:
;    APPLICANT:  Maggio, John E.
;    APPLICANT:  Mantyh, Patrick W.
;    TITLE OF INVENTION:  LABELLED BETA-AMYLOID PEPTIDE AND
;    TITLE OF INVENTION:  METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  P.O. Box 581415
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55458-1415
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/304,585
;      FILING DATE:  12-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  110.00010120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1217
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-304-585-1

  Query Match             100.0%;  Score 55;  DB 1;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 40
US-08-302-808-3
; Sequence 3, Application US/08302808
; Patent No. 5750349
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5750349uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/302,808
;      FILING DATE:  15-SEP-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/00089
;      FILING DATE:  24-JAN-1994
;      APPLICATION NUMBER:  010132/1993
;      FILING DATE:  25-JAN-1993
;      APPLICATION NUMBER:  019035/1993
;      FILING DATE:  05-FEB-1993
;      APPLICATION NUMBER:  286985/1993
;      FILING DATE:  16-NOV-1993
;      APPLICATION NUMBER:  334773/1993
;      FILING DATE:  28-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  44631
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
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;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-302-808-3

  Query Match             100.0%;  Score 55;  DB 1;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 41
US-08-433-734-1
; Sequence 1, Application US/08433734
; Patent No. 5837473
;  GENERAL INFORMATION:
;    APPLICANT:  Maggio, John E.
;    APPLICANT:  Mantyh, Patrick W.
;    TITLE OF INVENTION:  Labelled  -Amyloid Peptide and Methods
;    TITLE OF INVENTION:  for Use in Detecting Alzheimer's Disease
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  P.O. Box 581415
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55458-1415
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/433,734
;      FILING DATE:  03-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  110.00010102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1220
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-433-734-1

  Query Match             100.0%;  Score 55;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 42
US-08-609-090-8
; Sequence 8, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,090
;      FILING DATE:  29-FEB-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kraus, Eric J.
;      REGISTRATION NUMBER:  36,190
;      REFERENCE/DOCKET NUMBER:  434-059
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-684-1111
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-609-090-8

  Query Match             100.0%;  Score 55;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 43
US-07-737-371E-69
; Sequence 69, Application US/07737371E
; Patent No. 5876948
;  GENERAL INFORMATION:
;    APPLICANT:  Yankner, Bruce A.
;    TITLE OF INVENTION:  SCREENING METHODS TO IDENTIFY
;    TITLE OF INVENTION:  NEUROTOXIN INHIBITORS (AS AMENDED)
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/737,371E
;      FILING DATE:  29-JUL-1991
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/559,172
;      FILING DATE:  27-JUL-1990
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  00108/028002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-737-371E-69

  Query Match           100.0%;  Score 55;  DB 2;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 44
US-08-682-245A-2
; Sequence 2, Application US/08682245A
; Patent No. 5919631
;  GENERAL INFORMATION:
;    APPLICANT:  GOYAL, SHEFALI
;    APPLICANT:  PAUL, JOSEPH W
;    APPLICANT:  RIEDEL, NORBERT G
;    APPLICANT:  SAHASRABUDHE, SUDHIR
;    TITLE OF INVENTION:  A METHOD OF DETERMINING THE DEGREE OF
;    TITLE OF INVENTION:  AGGREGATION OF THE BA4 PEPTIDE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOECHST MARION ROUSSEL, INC.
;      STREET:  2110 E. GALBRAITH RD., P.O. BOX 156300
;      CITY:  CINCINNATI
;      STATE:  OHIO
;      COUNTRY:  U.S.A.
;      ZIP:  45215-6300
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/682,245A
;      FILING DATE:  17-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,414
;      FILING DATE:  16-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LENTZ, NELSEN L
;      REGISTRATION NUMBER:  38,537
;      REFERENCE/DOCKET NUMBER:  HR-1257A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  513-948-7369
;      TELEFAX:  513-948-7961 OR 4681
;      TELEX:  214320
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-682-245A-2

  Query Match           100.0%;  Score 55;  DB 2;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 45
US-08-986-948-3
; Sequence 3, Application US/08986948
; Patent No. 5955317
;  GENERAL INFORMATION:
;    APPLICANT:  SUZUKI, No. 5955317uhiro
;    APPLICANT:  ODAKA, Asano
;    APPLICANT:  KITADA, Chieko
;    TITLE OF INVENTION:  ANTIBODIES TO B-AMYLOIDS OR THEIR
;    TITLE OF INVENTION:  DERIVATIVES AND USE THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02019
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/986,948
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/302,808
;      FILING DATE:  15-SEP-1994
;      APPLICATION NUMBER:  PCT/JP94/00089
;      FILING DATE:  24-JAN-1994
;      APPLICATION NUMBER:  010132/1993
;      FILING DATE:  25-JAN-1993
;      APPLICATION NUMBER:  019035/1993
;      FILING DATE:  05-FEB-1993
;      APPLICATION NUMBER:  286985/1993
;      FILING DATE:  16-NOV-1993
;      APPLICATION NUMBER:  334773/1993
;      FILING DATE:  28-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  44631
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
US-08-986-948-3

  Query Match           100.0%;  Score 55;  DB 2;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 46
US-08-461-216-1
; Sequence 1, Application US/08461216
; Patent No. 5958883
;  GENERAL INFORMATION:
;     APPLICANT:  Snow, A.D.
;     TITLE OF INVENTION:  ANIMAL MODELS OF HUMAN AMYLOIDOSES
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Christensen, O'Connor, Johnson and Kindness
;       STREET:  1420 Fifth Avenue, Suite 2800
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  USA
;       ZIP:  98101-2347
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette-5.25 inch, 1.2Mb storage
;       COMPUTER:  IBM PC/386 Compatible
;       OPERATING SYSTEM:  MS-DOS 4.01
;       SOFTWARE:  Word for Windows-t
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/461,216
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/969,734
;       FILING DATE:  October 23, 1992
;       APPLICATION NUMBER:  07/950,417
;       FILING DATE:  September 23, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Broderick, Thomas F.
;       REGISTRATION NUMBER:  31,332
;       REFERENCE/DOCKET NUMBER:  UOFW-1-6707
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  1-206-682-8100; 1-206-224-0709 (direct)
;       TELEFAX:  1-206-224-0779
;       TELEX:  4938023
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  40 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;       DESCRIPTION:  {SYMBOL 98 \f "Symbol"}/A4(1-40);
;       DESCRIPTION:  FIGURES 23-29
US-08-461-216-1

  Query Match             100.0%;  Score 55;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 47
US-08-959-148-1
; Sequence 1, Application US/08959148
; Patent No. 6172277
; GENERAL INFORMATION:
;  APPLICANT: Tate, Barbara A.
;  APPLICANT: Majocha, Ronald
;  APPLICANT: Newton, Julie L.
;  TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE
;  FILE REFERENCE: 04930/022001
;  CURRENT APPLICATION NUMBER: US/08/959,148
;  CURRENT FILING DATE: 1997-10-28
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-959-148-1

  Query Match             100.0%;  Score 55;  DB 4;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 48
US-09-242-724-22
; Sequence 22, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-242-724-22

  Query Match             100.0%;  Score 55;  DB 4;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 49
US-08-723-661B-1
; Sequence 1, Application US/08723661B
; Patent No. 6340783
;   GENERAL INFORMATION:
;        APPLICANT: Alan D Snow
;        TITLE OF INVENTION: Animal Models of Human Amyloidoses
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Patrick M. Dwyer
;             STREET: 1818 Westlake Avenue N, Suite 114
;             CITY: Seattle
;             STATE: WA (Washington)
;             COUNTRY: United States of America
;             ZIP: 98109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
;             COMPUTER: IBM PC
;             OPERATING SYSTEM: PC-DOS (Windows 98)
;             SOFTWARE: WordPerfect 5.2
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/723,661B
;             FILING DATE: 31-Oct-1996
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/461,216
;             FILING DATE: 05-Jun-1995
```

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;             APPLICATION NUMBER: 07/969,734
;             FILING DATE: 23-Oct-1992
;             APPLICATION NUMBER: 07/950,417
;             FILING DATE: 23-Sep-1992
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Dwyer, Patrick M.
;             REGISTRATION NUMBER: 32,411
;             REFERENCE/DOCKET NUMBER: PROTEO.P00C1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 343-7074
;             TELEFAX: (206) 343-7085
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 40 AMINO ACIDS
;             TYPE: AMINO ACID
;             STRANDEDNESS: SINGLE
;             TOPOLOGY: LINEAR
;       MOLECULE TYPE: PEPTIDE
;             DESCRIPTION: /A4 (1-40); FIGURES 23-29
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-723-661B-1

  Query Match            100.0%;  Score 55;  DB 4;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22


RESULT 50
PCT-US92-06700-1
; Sequence 1, Application PC/TUS9206700
;  GENERAL INFORMATION:
;    APPLICANT:  Mantyh, Patrick W.
;    APPLICANT:  Maggio, John E.
;    TITLE OF INVENTION:  Labelled  -Amyloid Peptide
;    TITLE OF INVENTION:  and Alzheimer's Disease Detection
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 Norwest Center
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 720 Kb
;      COMPUTER:  Northgate 386
;      OPERATING SYSTEM:  DOS 4.0
;      SOFTWARE:  WordPerfect  5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06700
;      FILING DATE:  19920810
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kowalchyk, Alan W.
;      REGISTRATION NUMBER:  31,535
;      REFERENCE/DOCKET NUMBER:  600.226-WO-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (612) 332-5300
;      TELEFAX:  (612) 332-9081
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acid residues
;      TYPE:  AMINO ACID
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Peptide
;    FRAGMENT TYPE:  Internal Fragment
;    ORIGINAL SOURCE:  Synthetically Derived
;    FEATURE:
;      NAME/KEY:  Internal fragment of the  -
;      NAME/KEY:  amyloid peptide precursor
;      LOCATION:  Represents isolated internal
;      LOCATION:  sequence of 40 amino acid residues from
;      LOCATION:  the  -amyloid peptide precursor
PCT-US92-06700-1

  Query Match            100.0%;  Score 55;  DB 5;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 0.00037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22


Search completed: October 29, 2002, 09:25:38
Job time : 14 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:27 ; Search time 16 Seconds
(without alignments)
60.056 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	42	2	PN0512	beta-amyloid prote
2	55	100.0	57	2	E60045	Alzheimer's diseas
3	55	100.0	57	2	F60045	Alzheimer's diseas
4	55	100.0	57	2	G60045	Alzheimer's diseas
5	55	100.0	57	2	D60045	Alzheimer's diseas
6	55	100.0	57	2	A60045	Alzheimer's diseas
7	55	100.0	57	2	B60045	Alzheimer's diseas
8	55	100.0	82	2	PQ0438	Alzheimer's diseas
9	55	100.0	695	1	A49795	Alzheimer's diseas
10	55	100.0	747	2	JH0773	Alzheimer's diseas
11	55	100.0	770	1	QRHUA4	Alzheimer's diseas
12	47	85.5	33	2	S23094	beta-amyloid prote
13	47	85.5	695	2	A27485	Alzheimer's diseas
14	47	85.5	695	2	S00550	Alzheimer's diseas
15	39	70.9	699	2	H64118	4-alpha-glucanotra
16	38	69.1	272	2	F70979	hypothetical prote
17	38	69.1	549	1	NUEC	glucose-6-phosphat
18	38	69.1	549	2	H91254	glucosephosphate i
19	38	69.1	549	2	D86095	glucosephosphate i
20	38	69.1	549	2	AD1013	glucose-6-phosphat
21	38	69.1	550	2	B82330	glucose-6-phosphat
22	37	67.3	191	2	T04853	hypothetical prote
23	36	65.5	210	2	I58391	sarcoma amplified
24	36	65.5	535	2	S51577	transposase - rice
25	36	65.5	859	2	F69159	protoporphyrin IX
26	36	65.5	1668	1	C69224	cobalamin biosynth
27	35	63.6	297	2	T23909	hypothetical prote
28	35	63.6	446	2	T50786	nucleoid DNA-bindi
29	35	63.6	549	2	G84996	glucose-6-phosphat
30	35	63.6	552	2	T25496	hypothetical prote
31	35	63.6	751	2	D71860	probable outer mem
32	35	63.6	850	2	JC5047	ras GTPase-activat
33	35	63.6	2347	1	TVHURS	kinase-related pro
34	34	61.8	124	1	B54546	small peptidoglyca
35	34	61.8	140	2	C81176	hypothetical prote
36	34	61.8	270	2	AG1727	unkown protein hom
37	34	61.8	281	2	AG1357	unkown proteins ho
38	34	61.8	590	2	F95853	probable phospholi
39	34	61.8	635	2	H81793	hypothetical prote
40	34	61.8	763	2	S51300	probable membrane
41	34	61.8	1163	2	S07137	DNA-directed RNA p
42	34	61.8	1356	2	S51389	ROM2 protein - yea
43	34	61.8	1375	2	T18961	FAB1 protein homol
44	34	61.8	4427	2	PN0637	polyketide synthas
45	33	60.0	214	2	S39644	acetoin utilizatio
46	33	60.0	255	2	S41511	Brn-3a protein - m
47	33	60.0	258	2	D72217	conserved hypothet
48	33	60.0	325	2	A47003	cytokine receptor
49	33	60.0	334	2	T20562	hypothetical prote
50	33	60.0	336	2	S32170	phytoene synthetas

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
A;Reference number: PN0512; MUID:93290653
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 55; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22
```

RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A;Reference number: A60045; MUID:92017079
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 55; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 HHQKLVFFAE 10
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```
          ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 3
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             100.0%;  Score 55;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             100.0%;  Score 55;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             100.0%;  Score 55;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A;Reference number: A60045; MUID:92017079
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             100.0%;  Score 55;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A;Reference number: A60045; MUID:92017079
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             100.0%;  Score 55;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A;Reference number: PQ0438; MUID:93075180
A;Accession: PQ0438
A;Molecule type: DNA
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A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 55; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 29 HHQKLVFFAE 38

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A;Reference number: A49795; MUID:91273117
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing

Query Match 100.0%; Score 55; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 609 HHQKLVFFAE 618

RESULT 10
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 100.0%; Score 55; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 661 HHQKLVFFAE 670

RESULT 11
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inh
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252;
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode
A;Reference number: S02260; MUID:89128427
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-pr
A;Reference number: A32277; MUID:89165870
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
A;Reference number: A33260; MUID:89392030
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A;Reference number: A35486; MUID:90321244
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168
A;Contents: annotation; erratum

A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheime
A;Reference number: I59562; MUID:92022553
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A;Reference number: A03134; MUID:87144572
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
A;Reference number: S02638; MUID:88296437
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A;Reference number: S00707; MUID:88122640
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhi
A;Reference number: S00925; MUID:88122639
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
A;Reference number: A38949; MUID:88122641
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A;Reference number: A31087; MUID:88124954
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther,

Query Match 100.0%; Score 55; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    684 HHQKLVFFAE 693
```

```
RESULT 12
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A;Reference number: S23094; MUID:92316198
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

  Query Match             85.5%;  Score 47;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.0099;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           |||||||||
Db      19 HQKLVFFAE 27


RESULT 13
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A;Reference number: A27485; MUID:88106489
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A;Reference number: I49485; MUID:92209998
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid; transmembrane protein

  Query Match             85.5%;  Score 47;  DB 2;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           |||||||||
Db     610 HQKLVFFAE 618


RESULT 14
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br
A;Reference number: S00550; MUID:88312583
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co
A;Reference number: A41245; MUID:88264430
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
A;Reference number: A39820; MUID:91217087
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

  Query Match             85.5%;  Score 47;  DB 2;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           |||||||||
Db     610 HQKLVFFAE 618


RESULT 15
H64118
4-alpha-glucanotransferase homolog - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: H64118
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
A;Accession: H64118
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-699 <TIGR>
A;Cross-references: GB:U32815; GB:L42023; NID:g1574818; PIDN:AAC23003.1; PID:g1574819
C;Genetics:
A;Start codon: GTG
C;Superfamily: 4-alpha-glucanotransferase
```

```
  Query Match             70.9%;  Score 39;  DB 2;  Length 699;
  Best Local Similarity   66.7%;  Pred. No. 9.5;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           ||:|: |||
Db     349 HHEKIQFFA 357


RESULT 16
F70979
hypothetical protein Rv3277 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70979
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987
A;Accession: F70979
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-272 <COL>
A;Cross-references: GB:Z92771; GB:AL123456;*NID:g3242259; PIDN:CAB07080.1; PID:e306544;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3277

  Query Match             69.1%;  Score 38;  DB 2;  Length 272;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           ||: |:|||
Db     137 HHEALLFFA 145


RESULT 17
NUEC
glucose-6-phosphate isomerase (EC 5.3.1.9) - Escherichia coli
N;Alternate names: phosphoglucose isomerase; phosphohexose isomerase
C;Species: Escherichia coli
C;Date: 31-Mar-1990 #sequence_revision 17-Oct-1997 #text_change 08-Sep-2000
C;Accession: H65209; JS0142; S04396
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: H65209
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-549 <BLAT>
A;Cross-references: GB:AE000476; GB:U00096; NID:g1790456; PIDN:AAC76995.1; PID:g1790457;
A;Experimental source: strain K-12, substrain MG1655
R;Froman, B.E.; Tait, R.C.; Gottlieb, L.D.
Mol. Gen. Genet. 217, 126-131, 1989
A;Title: Isolation and characterization of the phosphoglucose isomerase gene from Escher
A;Reference number: JS0142; MUID:89364675
A;Accession: JS0142
A;Molecule type: DNA
A;Residues: 1-316,'V',318-549 <FRO>
A;Cross-references: GB:X15196; NID:g42376; PIDN:CAA33268.1; PID:g42377
A;Experimental source: strain JM101
A;Note: the authors translated the codon CAG for residue 8 as Trp
C;Comment: This enzyme catalyzes the reversible isomerization of glucose-6-phosphate and
C;Genetics:
A;Gene: pgi
A;Map position: 91 min
C;Superfamily: glucose-6-phosphate isomerase
C;Keywords: glycolysis; homodimer; intramolecular oxidoreductase; isomerase
F;514/Active site: Lys #status predicted

  Query Match             69.1%;  Score 38;  DB 1;  Length 549;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     416 HHQKLLSNFFAQ 427


RESULT 18
H91254
glucosephosphate isomerase [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: H91254
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91254
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB38431.1; PID:g13364485; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs5008
C;Superfamily: glucose-6-phosphate isomerase

  Query Match             69.1%;  Score 38;  DB 2;  Length 549;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     416 HHQKLLSNFFAQ 427


RESULT 19
D86095
glucosephosphate isomerase [imported] - Escherichia coli (strain O157:H7, substrain E
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D86095
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D86095
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <STO>
A;Cross-references: GB:AE005174; NID:g12518968; PIDN:AAG59224.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: pgi
C;Superfamily: glucose-6-phosphate isomerase

  Query Match             69.1%;  Score 38;  DB 2;  Length 549;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     416 HHQKLLSNFFAQ 427


RESULT 20
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```
AD1013
glucose-6-phosphate isomerase (EC 5.3.1.9) [imported] - Salmonella enterica subsp. enter
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1013
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AD1013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09205.1; PID:g16505209; GSPDB:GN00176
C;Genetics:
A;Gene: STY4417
C;Superfamily: glucose-6-phosphate isomerase
C;Keywords: intramolecular oxidoreductase; isomerase

  Query Match             69.1%;  Score 38;  DB 2;  Length 549;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     416 HHQKLLSNFFAQ 427


RESULT 21
B82330
glucose-6-phosphate isomerase VC0374 [imported] - Vibrio cholerae (strain N16961 serogrc
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82330
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: B82330
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-550 <HEI>
A;Cross-references: GB:AE004126; GB:AE003852; NID:g9654802; PIDN:AAF93547.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0374
A;Map position: 1
C;Superfamily: glucose-6-phosphate isomerase

  Query Match             69.1%;  Score 38;  DB 2;  Length 550;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     417 HHQKLMSNFFAQ 428


RESULT 22
T04853
hypothetical protein F28A21.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C;Accession: T04853
R;Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15387
A;Accession: T04853
A;Molecule type: DNA
A;Residues: 1-191 <BEV>
A;Cross-references: EMBL:AL035526
A;Experimental source: cultivar Columbia; BAC clone F28A21
C;Genetics:
A;Map position: 4
A;Note: F28A21.20
C;Superfamily: Arabidopsis thaliana hypothetical protein F28A21.20

  Query Match             67.3%;  Score 37;  DB 2;  Length 191;
  Best Local Similarity   60.0%;  Pred. No. 6.1;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           |||  ||| :
Db      86 HHQACVFFGQ 95


RESULT 23
I58391
sarcoma amplified sequence SAS [imported] - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C;Accession: I58391
R;Jankowski, S.A.; Mitchell, D.S.; Smith, S.H.; Trent, J.M.; Meltzer, P.S.
Oncogene 9, 1205-1211, 1994
A;Title: SAS, a gene amplified in human sarcomas, encodes a new member of the transme
A;Reference number: I58391; MUID:94181273
A;Accession: I58391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RES>
A;Cross-references: EMBL:U01160; NID:g457936; PIDN:AAA17782.1; PID:g457937
C;Genetics:
A;Gene: GDB:SAS
A;Cross-references: GDB:128054; OMIM:181035
A;Map position: 12q13-12q14

  Query Match             65.5%;  Score 36;  DB 2;  Length 210;
  Best Local Similarity   75.0%;  Pred. No. 11;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||| |:||
Db      70 HHQVLLFF 77


RESULT 24
S51577
transposase - rice blast fungus
C;Species: Magnaporthe grisea (rice blast fungus)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Sep-1997
C;Accession: S51577
R;Kachroo, P.; Leong, S.A.; Chattoo, B.B.
Mol. Gen. Genet. 245, 339-348, 1994
A;Title: Pot2, an inverted repeat transposon from the rice blast fungus Magnaporthe g
A;Reference number: S51577; MUID:95115685
A;Accession: S51577
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <KAC>
A;Cross-references: EMBL:Z33638; NID:g496853; PID:g496854

  Query Match             65.5%;  Score 36;  DB 2;  Length 535;
  Best Local Similarity   77.8%;  Pred. No. 29;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           ||:| ||||
Db      80 HQELRFFAE 88
```

RESULT 25
F69159
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) - Methanobacterium thermoautotrophic
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: F69159
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514
A;Accession: F69159
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-859 <MTH>
A;Cross-references: GB:AE000830; GB:AE000666; NID:g2621523; PIDN:AAB84962.1; PID:g262152
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH456
C;Keywords: lyase

  Query Match 65.5%; Score 36; DB 2; Length 859;
  Best Local Similarity 66.7%; Pred. No. 47;
  Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
  ||| | |:|
Db 210 HHQYLAFYA 218

RESULT 26
C69224
cobalamin biosynthesis protein N - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: C69224
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514
A;Accession: C69224
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1668 <MTH>
A;Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AAB85426.1; PID:g262202
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH928
A;Start codon: GTG
C;Superfamily: Methanobacterium thermoautotrophicum cobalamin biosynthesis protein N

  Query Match 65.5%; Score 36; DB 1; Length 1668;
  Best Local Similarity 66.7%; Pred. No. 94;
  Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
  ||| | |:|
Db 792 HHQYLAFYA 800

RESULT 27
T23909
hypothetical protein R04F11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23909
R;Harris, B.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19816
A;Accession: T23909
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-297 <WIL>
A;Cross-references: EMBL:Z74475; PIDN:CAA98959.1; GSPDB:GN00023; CESP:R04F11.1
A;Experimental source: clone R04F11
C;Genetics:
A;Gene: CESP:R04F11.1
A;Map position: 5
A;Introns: 44/3; 82/3; 120/1; 156/1; 244/3

  Query Match 63.6%; Score 35; DB 2; Length 297;
  Best Local Similarity 55.6%; Pred. No. 24;
  Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
  ||: ::|||
Db 157 HHKGVIFFA 165

RESULT 28
T50786
nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50786
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.;
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
A;Accession: T50786
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-446 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 31/3; 173/1
A;Note: T30N20_40

  Query Match 63.6%; Score 35; DB 2; Length 446;
  Best Local Similarity 75.0%; Pred. No. 37;
  Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HHQKLVFF 8
  || ||||
Db 21 HHHHLVFF 28

RESULT 29
G84996
glucose-6-phosphate isomerase (EC 5.3.1.9) [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G84996
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A;Reference number: A84930; MUID:20445173
A;Accession: G84996
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: pgi; BU573
C;Superfamily: glucose-6-phosphate isomerase
C;Keywords: intramolecular oxidoreductase; isomerase

  Query Match 63.6%; Score 35; DB 2; Length 549;
  Best Local Similarity 58.3%; Pred. No. 47;
  Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

```
Qy       1 HHQKLV--FFAE 10
           || ||: · |||:
Db     416 HHMKLISNFFAQ 427


RESULT 30
T25496
hypothetical protein C03G6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25496
R;Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C03G6.
A;Reference number: Z20042
A;Accession: T25496
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-552 <MUR>
A;Cross-references: EMBL:U97008; PIDN:AAB52305.1; GSPDB:GN00023; CESP:C03G6.5
A;Experimental source: strain Bristol N2; clone C03G6
C;Genetics:
A;Gene: CESP:C03G6.5
A;Map position: 5
A;Introns: 28/3; 75/3; 213/3; 330/1; 393/3

  Query Match             63.6%;  Score 35;  DB 2;  Length 552;
  Best Local Similarity   66.7%;  Pred. No. 47;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           | ||::|||
Db     454 HTQKMLFFA 462


RESULT 31
D71860
probable outer membrane protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: D71860
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557
A;Accession: D71860
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-751 <ARN>
A;Cross-references: GB:AE001529; GB:AE001439; NID:g4155590; PIDN:AAD06586.1; PID:g415559
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp1008

  Query Match             63.6%;  Score 35;  DB 2;  Length 751;
  Best Local Similarity   77.8%;  Pred. No. 65;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           ||| ||| |
Db      26 HQKDVFFVE 34


RESULT 32
JC5047
ras GTPase-activating protein - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
C;Accession: JC5047
R;Kobayashi, M.; Masui, T.; Kusuda, J.; Kameoka, Y.; Hashimoto, K.; Iwashita, S.
Gene 175, 173-177, 1996
A;Title: Human rasGTPase-activating protein (human counterpart of GAP1m): Sequence of
A;Reference number: JC5047; MUID:97074668
A;Accession: JC5047
A;Molecule type: mRNA
A;Residues: 1-850 <KOB>
A;Cross-references: DDBJ:D78155; NID:g1060908; PIDN:BAA11230.1; PID:d1011892; PID:g10
C;Comment: This protein plays a role in the regulation of cell growth and differentat
C;Genetics:
A;Gene: GAP1m
A;Map position: 3q24-26
C;Superfamily: pleckstrin repeat homology; ras-specific GAP catalytic domain homology
F;356-568/Domain: ras-specific GAP catalytic domain homology <GAP>
F;603-704/Domain: pleckstrin repeat homology <PLK>

  Query Match             63.6%;  Score 35;  DB 2;  Length 850;
  Best Local Similarity   77.8%;  Pred. No. 74;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           || ||| ||
Db     370 HHDKLVPFA 378


RESULT 33
TVHURS
kinase-related protein ros-1 precursor - human
N;Alternate names: protein-tyrosine kinase mcf3 (activated ros-1)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) ros-1
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 11-Jun-1999
C;Accession: A35512; A25223; A24421; A33081
R;Birchmeier, C.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 4799-4803, 1990
A;Title: Characterization of ROS1 cDNA from a human glioblastoma cell line.
A;Reference number: A35512; MUID:90280463
A;Accession: A35512
A;Molecule type: mRNA
A;Residues: 1-2212,'N',2214-2227,'QC',2229-2347 <BIR>
A;Cross-references: GB:M34353
A;Experimental source: glioblastoma cell line SW-1088
R;Matsushime, H.; Wang, L.H.; Shibuya, M.
Mol. Cell. Biol. 6, 3000-3004, 1986
A;Title: Human c-ros-1 gene homologous to the v-ros sequence of UR2 sarcoma virus enc
A;Reference number: A25223; MUID:87064611
A;Accession: A25223
A;Molecule type: DNA
A;Residues: 1790-2245,'KFDSSEFSSFRCTVN' <MA2>
A;Cross-references: GB:M13368
A;Experimental source: placenta
A;Note: the differences after residue 2245 result from the authors' misinterpretation
R;Birchmeier, C.; Birnbaum, D.; Waitches, G.; Fasano, O.; Wigler, M.
Mol. Cell. Biol. 6, 3109-3116, 1986
A;Title: Characterization of an activated human ros gene.
A;Reference number: A24421; MUID:87064625
A;Accession: A24421
A;Molecule type: mRNA
A;Residues: 1854-2261,'A',2263-2347 <BI2>
A;Cross-references: GB:M13880; NID:g337482; PIDN:AAA36580.1; PID:g337483
A;Experimental source: tumor cells
A;Note: the mcf3 oncogene was formed by DNA rearrangement involving fusion of at leas
C;Genetics:
A;Gene: GDB:ROS1
A;Cross-references: GDB:120351; OMIM:165020
A;Map position: 6q22-6q22
A;Introns: 1853/1; 1881/1; 1926/2; 1980/3; 2002/2; 2045/3; 2078/2; 2145/2; 2190/2
C;Superfamily: kinase-related protein ros; LDL receptor YWTD-containing repeat homolo
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote
F;1-36/Domain: signal sequence #status predicted <SIG>
F;37-2347/Product: kinase-related protein ROS1 #status predicted <MAT>
F;37-1859/Domain: extracellular #status predicted <EXT>
F;335-378/Domain: LDL receptor YWTD-containing repeat homology <YW1>
F;466-503/Domain: LDL receptor YWTD-containing repeat homology <YWA>
```

F;715-757/Domain: LDL receptor YWTD-containing repeat homology <YW2>
F;758-798/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;799-838/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;843-888/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;893-933/Domain: LDL receptor YWTD-containing repeat homology <YW6>
F;1532-1574/Domain: LDL receptor YWTD-containing repeat homology <YW7>
F;1860-1883/Domain: transmembrane #status predicted <TMN>
F;1884-2347/Domain: intracellular #status predicted <INT>
F;1943-2222/Domain: protein kinase homology <KIN>
F;1951-1959/Region: protein kinase ATP-binding motif
F;52,114,123,324,352,471,607,628,706,714,732,939,961,1015,1087,1090,1211,1272,1330,1458,
F;1980/Active site: Lys #status predicted
F;2110,2114,2115/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat

Query Match 63.6%; Score 35; DB 1; Length 2347;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKLVFFAE 10
||::|:|:|
Db 333 HQQIVYFSE 341

RESULT 34
B54546
small peptidoglycan-associated lipoprotein slp precursor - Bacillus subtilis
N;Alternate names: PAL-related lipoprotein; peptidoglycan-associated lipoprotein homolog
C;Species: Bacillus subtilis
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Jun-2000
C;Accession: B54546; D69708
R;Hemilae, H.
FEMS Microbiol. Lett. 66, 37-41, 1991
A;Title: Sequence of a PAL-related lipoprotein from Bacillus subtilis.
A;Reference number: A54546; MUID:92038903
A;Accession: B54546
A;Molecule type: DNA
A;Residues: 1-124 <HEM>
A;Experimental source: 168 strain BRB1
A;Note: sequence extracted from NCBI backbone (NCBIN:63826, NCBIP:63828)
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033
A;Accession: D69708
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-124 <KUN>
A;Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13335.1; PID:g2633833
A;Experimental source: strain 168
C;Genetics:
A;Gene: slp
C;Superfamily: Bacillus subtilis small peptidoglycan-associated lipoprotein slp
C;Keywords: blocked amino end; lipoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
F;19/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 61.8%; Score 34; DB 1; Length 124;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
|| :::||::
Db 36 HHTQILFFSD 45

RESULT 35
C81176
hypothetical protein NMB0648 [imported] - Neisseria meningitidis (strain MC58 serogro
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: C81176
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
A;Accession: C81176
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <TET>
A;Cross-references: GB:AE002419; GB:AE002098; NID:g7225863; PIDN:AAF41069.1; PID:g722
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0648
C;Superfamily: Neisseria meningitidis hypothetical protein NMB0648

Query Match 61.8%; Score 34; DB 2; Length 140;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HHQKLVFF 8
|| |::|:
Db 86 HHDKVIFY 93

RESULT 36
AG1727
unkown protein homolog lin2364 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AG1727
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1727
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-270 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97591.1; PID:g16414887; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2364
C;Superfamily: hypothetical protein ywpJ

Query Match 61.8%; Score 34; DB 2; Length 270;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
|| :| |||
Db 72 HHPRLTTFAE 81

RESULT 37
AG1357
unkown proteins homolog lmo2263 [imported] - Listeria monocytogenes (strain EGD-e)

```
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1357
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1357
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-281 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00341.1; PID:g16411733; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2263

  Query Match             61.8%;  Score 34;  DB 2;  Length 281;
  Best Local Similarity   60.0%;  Pred. No. 37;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           || :|  |||
Db      83 HHPRLTTFAE 92


RESULT 38
F95853
probable phospholipase protein [imported] - Sinorhizobium meliloti (strain 1021) magapla
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F95853
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95853
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC48494.1; PID:g15139966; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb20094
A;Genome: plasmid

  Query Match             61.8%;  Score 34;  DB 2;  Length 590;
  Best Local Similarity   100.0%;  Pred. No. 79;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||||
Db     208 HHQKLV 213


RESULT 39
H81793
hypothetical protein NMA2205 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81793
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491
A;Reference number: A81775; MUID:20222556
A;Accession: H81793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-635 <PAR>
A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85416.1; PID:g738
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA2205

  Query Match             61.8%;  Score 34;  DB 2;  Length 635;
  Best Local Similarity   62.5%;  Pred. No. 86;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||| |::|
Db     387 HHQDLIWF 394


RESULT 40
S51300
probable membrane protein YNL311c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0376
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S51300; S59569; S63292; S63284
R;Nicaud, J.J.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 13.9 Kb fragment of yeast chromosome XIV identi
A;Reference number: S51285
A;Accession: S51300
A;Molecule type: DNA
A;Residues: 1-763 <NIC>
A;Cross-references: EMBL:Z46259; NID:g633655; PID:g633671
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 1077-1085, 1995
A;Title: Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV identifies
A;Reference number: S59562; MUID:96076632
A;Accession: S59569
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-763 <MAF>
A;Cross-references: EMBL:Z46259; NID:g633655; PIDN:CAA86384.1; PID:g633671
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63292
A;Molecule type: DNA
A;Residues: 1-763 <MAW>
A;Cross-references: EMBL:Z71587; NID:g1302414; PID:g1302415; MIPS:YNL311c
A;Experimental source: strain S288C
R;Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63266
A;Accession: S63284
A;Molecule type: DNA
A;Residues: 148-763 <MAU>
A;Cross-references: EMBL:Z71587; MIPS:YNL311c
A;Experimental source: strain S288C
C;Genetics:
A;Map position: 14L
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YNL311c
C;Keywords: transmembrane protein
F;64-80/Domain: transmembrane #status predicted <TMM>

  Query Match             61.8%;  Score 34;  DB 2;  Length 763;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       1 HHQKLV 6
           ||||||
Db     323 HHQKLV 328


RESULT 41
S07137
DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - garden pea chloroplast (fragmen
C;Species: chloroplast Pisum sativum (garden pea)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1999
C;Accession: S07137
R;Cozens, A.L.; Walker, J.E.
Biochem. J. 236, 453-460, 1986
A;Title: Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal subunit S2
A;Reference number: S07137; MUID:86323089
A;Accession: S07137
A;Molecule type: DNA
A;Residues: 1-1163 <COZ>
A;Cross-references: EMBL:X03912; NID:g12137; PIDN:CAA27545.1; PID:g829325
C;Genetics:
A;Gene: rpoC2
A;Genome: chloroplast
C;Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription

  Query Match           61.8%;  Score 34;  DB 2;  Length 1163;
  Best Local Similarity  66.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           ||:||: ||
Db    1149 HHRKLLDFA 1157


RESULT 42
S51389
ROM2 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L8039.3; protein YLR371w
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999
C;Accession: S51389
R;Du, Z.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmid 8039.
A;Reference number: S51377
A;Accession: S51389
A;Molecule type: DNA
A;Residues: 1-1356 <DUZ>
A;Cross-references: EMBL:U19103; NID:g609404; PID:g609407; GSPDB:GN00012; MIPS:YLR371w
C;Genetics:
A;Gene: ROM2; MIPS:YLR371w
A;Map position: 12R
C;Superfamily: CDC24 homology
F;659-846/Domain: CDC24 homology <CD24>

  Query Match           61.8%;  Score 34;  DB 2;  Length 1356;
  Best Local Similarity  50.0%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    4;  Gaps    1;

Qy       1 HHQKLV----FFAE 10
           ||::|:    ||||
Db    1131 HHKELINHVSFFAE 1144


RESULT 43
T18961
FAB1 protein homolog VF11C1L.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18961; T26005
R;Lloyd, C.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19052
A;Accession: T18961
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1375 <WIL>
A;Cross-references: EMBL:Z67879; PIDN:CAA91791.1; GSPDB:GN00028; CESP:VF11C1L.1
A;Experimental source: clone C05E7
R;Mortimore, B.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z20126
A;Accession: T26005
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1375 <WI2>
A;Cross-references: EMBL:AL023817; PIDN:CAA19436.1; GSPDB:GN00028; CESP:VF11C1L.1
A;Experimental source: clone VF11C1L
C;Genetics:
A;Gene: CESP:VF11C1L.1
A;Map position: X
A;Introns: 109/1; 172/2; 198/3; 396/3; 561/3; 592/2; 647/1; 789/2; 859/3; 1104/3; 123

  Query Match           61.8%;  Score 34;  DB 2;  Length 1375;
  Best Local Similarity  75.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFA 9
           |:|| |||
Db     840 HEKLYFFA 847


RESULT 44
PN0637
polyketide synthase pksL - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 19-May-1994 #sequence_revision 06-Feb-1995 #text_change 03-Nov-2000
C;Accession: S25021; PN0637; B69679
R;Scotti, C.; Piatti, M.; Cuzzoni, A.; Tognoni, A.; Grandi, G.; Galizzi, A.; Albertin
submitted to the EMBL Data Library, July 1992
A;Description: A Bacillus subtilis large ORF coding for a polypeptide highly similar
A;Reference number: S25021
A;Accession: S25021
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4427 <SCO>
A;Cross-references: EMBL:Z14098; NID:g40057; PIDN:CAA78479.1; PID:g40058
R;Scotti, C.; Piatti, M.; Cuzzoni, A.; Perani, P.; Tognoni, A.; Grandi, G.; Galizzi,
Gene 130, 65-71, 1993
A;Title: A Bacillus subtilis large ORF coding for a polypeptide highly similar to pol
A;Reference number: PN0637; MUID:93345824
A;Accession: PN0637
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 184-282;382-850;926-1115;1409-1648;1665-1761;1876-2344;2469-2560;2609-270
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A69580; MUID:98044033
A;Accession: B69679
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-4427 <KUN>
```

```
A;Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13602.1; PID:g2634102
A;Experimental source: strain 168
C;Comment: This enzyme is composed of four synthase units. Unit1 comprises beta-ketosynt
acyl-carrier protein domains. Unit3 comprises beta-ketosynthase, acyl-carrier protein an
C;Genetics:
A;Gene: pksL; pksx
C;Superfamily: Bacillus subtilis polyketide synthase pksL; 3-oxoacyl-[acyl-carrier-prote
C;Keywords: acyltransferase; carrier protein
F;343-758/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F;1410-1591/Domain: short-chain alcohol dehydrogenase homology <SAD1>
F;1836-2252/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F;2485-2559/Domain: acyl carrier protein homology <ACP1>
F;2626-2700/Domain: acyl carrier protein homology <ACP2>
F;2783-3181/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
F;3576-3774/Domain: short-chain alcohol dehydrogenase homology <SAD2>
F;3852-3922/Domain: acyl carrier protein homology <ACP3>
F;3992-4372/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>

  Query Match             61.8%;  Score 34;  DB 2;  Length 4427;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||||
Db     691 HHQKLV 696


RESULT 45
S39644
acetoin utilization protein acuB - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 08-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S39644; D69582
R;Grundy, F.J.; Waters, D.A.; Takova, T.Y.; Henkin, T.M.
Mol. Microbiol. 10, 259-271, 1993
A;Title: Identification of genes involved in utilization of acetate and acetoin in Bacil
A;Reference number: S39641; MUID:95020526
A;Accession: S39644
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <GRU>
A;Cross-references: GB:L17309; NID:g861173; PIDN:AAA68285.1; PID:g348051
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033
A;Accession: D69582
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-214 <KUN>
A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14948.1; PID:e1185843;
A;Experimental source: strain 168
C;Genetics:
A;Gene: acuB

  Query Match             60.0%;  Score 33;  DB 2;  Length 214;
  Best Local Similarity   83.3%;  Pred. No. 43;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           |||||:
Db     110 HHQKLI 115


RESULT 46
S41511
Brn-3a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: S41511
R;Theil, T.; McLean-Hunter, S.; Zoernig, M.; Moeroey, T.
Nucleic Acids Res. 21, 5921-5929, 1993
A;Title: Mouse BRN-3 family of POU transcription factors: a new aminoterminal domain
A;Reference number: S41511; MUID:94119691
A;Accession: S41511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-255 <THE>
C;Superfamily: unassigned homeobox proteins; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;110-180/Domain: POU domain homology <POU>
F;199-255/Domain: homeobox homology <HOX>

  Query Match             60.0%;  Score 33;  DB 2;  Length 255;
  Best Local Similarity   60.0%;  Pred. No. 52;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||::|  |||
Db     107 HHRELEAFAE 116


RESULT 47
D72217
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72217
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316
A;Accession: D72217
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <ARN>
A;Cross-references: GB:AE001812; GB:AE000512; NID:g4982302; PIDN:AAD36798.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1733
C;Superfamily: conserved hypothetical protein HI0072

  Query Match             60.0%;  Score 33;  DB 2;  Length 258;
  Best Local Similarity   50.0%;  Pred. No. 53;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||  : |||:
Db     140 HHSSMWFFAD 149


RESULT 48
A47003
cytokine receptor family class II protein CRF2-4 precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 01-Dec-2000
C;Accession: A47003; G01418
R;Lutfalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at 1
A;Reference number: A47003; MUID:93300510
A;Accession: A47003
```

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
A;Cross-references: GB:Z17227; NID:g393378; PIDN:CAA78933.1; PID:g393379
R;Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A;Reference number: G06935
A;Accession: G01418
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-123,'D',125-268,'VGRME' <LU2>
A;Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C;Genetics:
A;Gene: GDB:CRFB4; CRF2-4
A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21q; 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
C;Keywords: transmembrane protein

Query Match 60.0%; Score 33; DB 2; Length 325;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
|| |:||:
Db 274 HHNTLLFFS 282

RESULT 49
T20562
hypothetical protein F07H5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20562
R;Steward, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19292
A;Accession: T20562
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-334 <WIL>
A;Cross-references: EMBL:Z68314; PIDN:CAA92663.1; GSPDB:GN00020; CESP:F07H5.2
A;Experimental source: clone F07H5
C;Genetics:
A;Gene: CESP:F07H5.2
A;Map position: 2
A;Introns: 72/2; 146/3; 217/1; 280/3

Query Match 60.0%; Score 33; DB 2; Length 334;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKLVFFAE 10
|||:|||:
Db 195 QKLLFFAD 202

RESULT 50
S32170
phytoene synthetase - Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Mar-2001
C;Accession: S32170; S67951
R;Botella, J.; Murillo, F.; Ruiz-vazquez, R.
submitted to the EMBL Data Library, March 1993
A;Description: Nucleotide and deduced protein sequences of a carotenoid gene cluster in
A;Reference number: S32168
A;Accession: S32170
A;Molecule type: DNA
A;Residues: 1-336 <BOT>
A;Cross-references: EMBL:Z21955; NID:g577589; PIDN:CAA79957.1; PID:g288222
A;Experimental source: strain DK1050
R;Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
Eur. J. Biochem. 233, 238-248, 1995
A;Title: A cluster of structural and regulatory genes for light-induced carotenogenes
A;Reference number: S67950; MUID:96061955
A;Accession: S67951
A;Molecule type: DNA
A;Residues: 151-175;185-213 <BOW>
C;Genetics:
A;Start codon: GTG
C;Superfamily: Mycobacterium marinum phytoene synthase

Query Match 60.0%; Score 33; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
|| | |||
Db 23 HHAKSFFFA 31

Search completed: October 29, 2002, 09:24:30
Job time : 19 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:27 ; Search time 11 Seconds
(without alignments)
35.200 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	57	1	A4_PIG	Q29023 sus scrofa
2	55	100.0	57	1	A4_URSMA	Q29149 ursus marit
3	55	100.0	58	1	A4_CANFA	Q28280 canis famil
4	55	100.0	58	1	A4_RABIT	Q28748 oryctolagus
5	55	100.0	58	1	A4_SHEEP	Q28757 ovis aries
6	55	100.0	59	1	A4_BOVIN	Q28053 bos taurus
7	55	100.0	751	1	A4_SAISC	Q95241 saimiri sci
8	55	100.0	770	1	A4_HUMAN	P05067 homo sapien
9	47	85.5	770	1	A4_MOUSE	P12023 mus musculu
10	47	85.5	770	1	A4_RAT	P08592 rattus norv
11	39	70.9	699	1	MALQ_HAEIN	P45176 haemophilus
12	38	69.1	549	1	G6PI_ECOLI	P11537 escherichia
13	38	69.1	550	1	G6PI_VIBCH	Q9kuy4 vibrio chol
14	36	65.5	109	1	SAS_PIG	Q29257 sus scrofa
15	36	65.5	204	1	TNE6_HUMAN	O95857 homo sapien
16	36	65.5	210	1	SAS_HUMAN	Q12999 homo sapien
17	35	63.6	549	1	G6PI_BUCAI	P57636 buchnera ap
18	35	63.6	549	1	G6PI_PASMU	Q9cnl2 pasteurella
19	35	63.6	849	1	RSG2_HUMAN	Q15283 homo sapien
20	35	63.6	2347	1	KROS_HUMAN	P08922 homo sapien
21	34	61.8	124	1	SLP_BACSU	P39910 bacillus su
22	34	61.8	763	1	YN51_YEAST	P42843 saccharomyc
23	34	61.8	1163	1	RPOD_PEA	P12227 pisum sativ
24	34	61.8	1356	1	ROM2_YEAST	P51862 saccharomyc
25	34	61.8	2715	1	TRX2_HUMAN	Q9umn6 homo sapien
26	34	61.8	4427	1	PKSL_BACSU	Q05470 bacillus su
27	33	60.0	214	1	ACUB_BACSU	P39066 bacillus su
28	33	60.0	258	1	PPNK_THEMA	Q9x255 thermotoga
29	33	60.0	325	1	I10S_HUMAN	Q08334 homo sapien
30	33	60.0	496	1	C7D9_SOYBN	O81971 glycine max
31	33	60.0	549	1	G6PI_HAEIN	P44312 haemophilus
32	33	60.0	564	1	SYT_MYCGE	P47615 mycoplasma
33	33	60.0	2150	1	SDC3_CAEEL	P34706 caenorhabdi
34	32	58.2	167	1	G6PI_KLEOX	P77877 klebsiella
35	32	58.2	178	1	CALC_MOUSE	Q63811 mus musculu
36	32	58.2	321	1	CYF_GUITH	O78494 guillardia
37	32	58.2	380	1	FD3E_SOYBN	P48625 glycine max
38	32	58.2	481	1	LBP_HUMAN	P18428 homo sapien
39	32	58.2	492	1	CPBJ_MOUSE	O55071 mus musculu
40	32	58.2	495	1	MURC_RICPR	Q9zds8 rickettsia
41	32	58.2	501	1	ACHB_MOUSE	P09690 mus musculu
42	32	58.2	517	1	ACHG_HUMAN	P07510 homo sapien
43	32	58.2	519	1	ACHG_BOVIN	P13536 bos taurus
44	32	58.2	519	1	ACHG_MOUSE	P04760 mus musculu
45	32	58.2	519	1	ACHG_RAT	P18916 rattus norv
46	32	58.2	557	1	PRXV_ASCNO	P81701 ascophyllum
47	32	58.2	616	1	YAWG_SCHPO	Q10190 schizosacch
48	32	58.2	734	1	GLGB_AGRTU	P52979 agrobacteri
49	32	58.2	808	1	PLD_PIMBR	O04883 pimpinella
50	32	58.2	808	1	PLD_RICCO	Q41142 ricinus com

ALIGNMENTS

RESULT 1
A4_PIG
ID A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC --

CC --
DR EMBL; X56127; CAA39592.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 55; DB 1; Length 57;

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  Best Local Similarity   100.0%;  Pred. No. 0.00019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     18 HHQKLVFFAE 27


RESULT 2
A4_URSMA
ID   A4_URSMA       STANDARD;      PRT;    57 AA.
AC   Q29149;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=29073;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56128; CAA39593.1; -.
DR   HSSP; P05067; 1AML.
DR   InterPro; IPR001868; A4_APP.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   NON_TER      57     57
SQ   SEQUENCE   57 AA;  6172 MW;  84209D88EBA82DFA CRC64;

  Query Match           100.0%;  Score 55;  DB 1;  Length 57;
  Best Local Similarity  100.0%;  Pred. No. 0.00019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     18 HHQKLVFFAE 27


RESULT 3
A4_CANFA
ID   A4_CANFA       STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

  Query Match           100.0%;  Score 55;  DB 1;  Length 58;
  Best Local Similarity  100.0%;  Pred. No. 0.0002;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     19 HHQKLVFFAE 28


RESULT 4
A4_RABIT
ID   A4_RABIT       STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
```

```
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             100.0%;  Score 55;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 5
A4_SHEEP
ID   A4_SHEEP       STANDARD;      PRT;    58 AA.
AC   Q28757;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56130; CAA39595.1; -.
DR   HSSP; P05067; 1AML.
DR   InterPro; IPR001868; A4_APP.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             100.0%;  Score 55;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      18 HHQKLVFFAE 27


RESULT 6
A4_BOVIN
ID   A4_BOVIN       STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
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FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             100.0%;  Score 55;  DB 1;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     19 HHQKLVFFAE 28


RESULT 7
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DE   amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver, and Kidney;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW   Signal; Serine protease inhibitor.
FT   SIGNAL        1    17       BY SIMILARITY.
FT   CHAIN        18   751       A4 PROTEIN.
FT   CHAIN       653   695       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       18   680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681   704       POTENTIAL.
FT   DOMAIN      705   751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      287   345       BPTI/KUNITZ INHIBITOR.
FT   SITE        740   743       CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE    301   302       REACTIVE BOND.
FT   DISULFID    291   341       BY SIMILARITY.
FT   DISULFID    300   324       BY SIMILARITY.
FT   DISULFID    316   337       BY SIMILARITY.
FT   CARBOHYD    523   523       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   CARBOHYD    552   552       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE  751 AA;  84893 MW;  6C3E431089569049 CRC64;

  Query Match             100.0%;  Score 55;  DB 1;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.0027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    665 HHQKLVFFAE 674


RESULT 8
A4_HUMAN
ID   A4_HUMAN       STANDARD;      PRT;   770 AA.
AC   P05067; P09000; Q16011;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
DE   (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP OR A4 OR CVAP OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT   cell-surface receptor.";
RL   Nature 325:733-736(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88122639; PubMed=2893289;
RA   Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA   Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA   Cordell B.;
RT   "A new A4 amyloid mRNA contains a domain homologous to serine
RT   proteinase inhibitors.";
RL   Nature 331:525-527(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89128427; PubMed=2783775;
RA   Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA   Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT   "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT   is encoded by 16 exons.";
RL   Nucleic Acids Res. 17:517-522(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97263807; PubMed=9108164;
RA   Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA   Saito M., Tsukuni S., Sakaki Y.;
RT   "A novel method for making nested deletions and its application for
```

RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [6]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [7]
RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [8]
RP SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
RP SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [10]
RP SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [11]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
RP SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RP IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RT the Kunitz domain is protease nexin-II.";
RL Nature 341:144-147(1989).
RN [14]
RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor.";
RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RP COMPLEX WITH G(O).
RX MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(o).";
RL Nature 362:75-79(1993).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=99215582; PubMed=10201399;
RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein.";
RL Nat. Struct. Biol. 6:327-331(1999).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor.";
RL Biochemistry 29:10018-10022(1990).
RN [18]
RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031488; PubMed=1718421;
RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kamarck M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein.";
RL Biochemistry 30:10467-10478(1991).
RN [19]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Talafous J., Marcinowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RL Biochemistry 33:7788-7796(1994).
RN [20]
RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment.";
RL Biochemistry 35:16094-16104(1996).
RN [21]
RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RT environment. Is the membrane-spanning domain where we think it is?";
RL Biochemistry 37:11064-11077(1998).
RN [22]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RL J. Struct. Biol. 130:142-152(2000).
RN [23]
RP STRUCTURE BY NMR OF 681-706.
RX MEDLINE=20400065; PubMed=10940221;
RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;

```
RT   "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RT   water.";
RL   J. Struct. Biol. 130:130-141(2000).
RN   [24]
RP   SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX   MEDLINE=88296437; PubMed=2900137;
RA   Dyrks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RA   Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT   "Identification, transmembrane orientation and biogenesis of the
RT   amyloid A4 precursor of Alzheimer's disease.";

  Query Match             100.0%;  Score 55;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.0027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db     684 HHQKLVFFAE 693


RESULT 9
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor
DE   (Amyloidogenic glycoprotein) (AG).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [2]
RP   SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [3]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   STRAIN=CD-1; TISSUE=Placenta;
RX   MEDLINE=89345111; PubMed=2569710;
RA   Fukuchi K., Martin G.M., Deeb S.S.;
RT   "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT   precursor of Mus domesticus.";
RL   Nucleic Acids Res. 17:5396-5396(1989).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=89149813; PubMed=2493250;
RA   Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT   "Structure and expression of the alternatively-spliced forms of mRNA
RT   for the mouse homolog of Alzheimer's disease amyloid beta protein
RT   precursor.";
RL   Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC       APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC       WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC       LIVER.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X59379; -; NOT_ANNOTATED_CDS.
DR   EMBL; M18373; AAA37139.1; -.
DR   EMBL; X15210; CAA33280.1; -.
DR   EMBL; D10603; BAA01456.1; -.
DR   EMBL; M24397; AAA39929.1; -.
DR   PIR; A27485; A27485.
DR   PIR; S04855; S04855.
DR   PIR; S19727; S19727.
DR   HSSP; P05067; 1QCM.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Alternative splicing; Serine protease inhibitor.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                HOMOLOG.
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      673    715       EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT   DOMAIN      287    345       BPTI/KUNITZ INHIBITOR.
FT   SITE        759    762       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    291    341       BY SIMILARITY.
FT   DISULFID    300    324       BY SIMILARITY.
FT   DISULFID    316    337       BY SIMILARITY.
FT   CARBOHYD    542    542       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    571    571       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    289    289       E -> V (IN ISOFORM APP(695)).
FT   VARSPLIC    290    364       MISSING (IN ISOFORM APP(695)).
FT   VARSPLIC    346    380       MISSING (IN ISOFORM APP(751)).
SQ   SEQUENCE   770 AA;  86752 MW;  26C50DE0890CAF7A CRC64;

  Query Match             85.5%;  Score 47;  DB 1;  Length 770;
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  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQKLVFFAE 10
          |||||||||
Db    685 HQKLVFFAE 693


RESULT 10
A4_RAT
ID   A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor
DE   (Amyloidogenic glycoprotein) (AG).
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC       APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC       SPLICING.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07648; CAA30488.1; -.
DR   EMBL; X14066; CAA32229.1; -.
DR   PIR; S00550; S00550.
DR   PIR; S03607; S03607.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Alternative splicing; Serine protease inhibitor.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                 HOMOLOG.
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      673    715       EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT   DOMAIN      287    345       BPTI/KUNITZ INHIBITOR.
FT   SITE        759    762       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    291    341       BY SIMILARITY.
FT   DISULFID    300    324       BY SIMILARITY.
FT   DISULFID    316    337       BY SIMILARITY.
FT   CARBOHYD    542    542       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    571    571       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    289    289       E -> V (IN ISOFORM APP(695)).
FT   VARSPLIC    290    364       MISSING (IN ISOFORM APP(695)).
SQ   SEQUENCE   770 AA;  86704 MW;  C26C9D6BB2D929A7 CRC64;

  Query Match             85.5%;  Score 47;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQKLVFFAE 10
          |||||||||
Db    685 HQKLVFFAE 693


RESULT 11
MALQ_HAEIN
ID   MALQ_HAEIN      STANDARD;      PRT;   699 AA.
AC   P45176;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
DE   (Disproportionating enzyme) (D-enzyme).
GN   MALQ OR HI1356.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RD / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus
RT   influenzae Rd.";
RL   Science 269:496-512(1995).
CC   -!- CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan
CC       to a new 4-position in an acceptor, which may be glucose or (1,4)-
CC       alpha-D-glucan.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE DISPROPORTIONATING ENZYME FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U32815; AAC23003.1; -.
DR   TIGR; HI1356; -.
DR   InterPro; IPR003385; 4A_glucanotrans.
DR   Pfam; PF02446; 4A_glucanotrans; 1.
KW   Transferase; Glycosyltransferase; Carbohydrate metabolism;
KW   Complete proteome.
SQ   SEQUENCE   699 AA;  80251 MW;  80D6E1D51EC2E1E9 CRC64;

  Query Match             70.9%;  Score 39;  DB 1;  Length 699;
  Best Local Similarity   66.7%;  Pred. No. 3.8;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           ||:|: |||
Db     349 HHEKIQFFA 357


RESULT 12
G6PI_ECOLI
ID   G6PI_ECOLI     STANDARD;      PRT;   549 AA.
AC   P11537;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN   PGI OR B4025 OR Z5623 OR ECS5008.
OS   Escherichia coli, and
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562, 83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JM101;
RX   MEDLINE=89364675; PubMed=2549364;
RA   Froman B.E., Tait R.C., Gottlieb L.D.;
RT   "Isolation and characterization of the phosphoglucose isomerase gene
RT   from Escherichia coli.";
RL   Mol. Gen. Genet. 217:126-131(1989).
RN   [2]
RP   SEQUENCE FROM N.A., AND PHYLOGENETIC STUDY.
RC   STRAIN=XL1 BLUE 2;
RX   MEDLINE=92277670; PubMed=1593646;
RA   Smith M.W., Doolittle R.F.;
RT   "Anomalous phylogeny involving the enzyme glucose-6-phosphate
RT   isomerase.";
RL   J. Mol. Evol. 34:544-545(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=94089392; PubMed=8265357;
RA   Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA   Daniels D.L.;
RT   "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT   region from 89.2 to 92.8 minutes.";
RL   Nucleic Acids Res. 21:5408-5417(1993).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
CC   -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC       phosphate.
CC   -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X15196; CAA33268.1; -.
DR   EMBL; U00006; AAC43119.1; -.
DR   EMBL; AE000476; AAC76995.1; -.
DR   EMBL; AE005635; AAG59224.1; -.
DR   EMBL; AP002568; BAB38431.1; -.
DR   PIR; JS0142; NUEC.
DR   EcoGene; EG10702; pgi.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW   Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT   ACT_SITE    386    386       BY SIMILARITY.
FT   ACT_SITE    514    514       BY SIMILARITY.
FT   CONFLICT    317    317       L -> V (IN REF. 1 AND 2).
SQ   SEQUENCE   549 AA;  61529 MW;  74AEDB670A068A01 CRC64;

  Query Match             69.1%;  Score 38;  DB 1;  Length 549;
  Best Local Similarity   66.7%;  Pred. No. 4.6;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     416 HHQKLLSNFFAQ 427


RESULT 13
G6PI_VIBCH
ID   G6PI_VIBCH     STANDARD;      PRT;   550 AA.
AC   Q9KUY4;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN   PGI OR VC0374.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EL TOR N16961 / SEROTYPE O1;
RX   MEDLINE=20406833; PubMed=10952301;
RA   Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA   Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA   Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA   Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA   McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
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RA   Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA   Fraser C.M.;
RT   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT   cholerae.";
RL   Nature 406:477-483(2000).
CC   -!- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE = FRUCTOSE 6-PHOSPHATE.
CC   -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE004125; AAF93547.1; -.
DR   TIGR; VC0374; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW   Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT   ACT_SITE    387    387       BY SIMILARITY.
FT   ACT_SITE    515    515       BY SIMILARITY.
SQ   SEQUENCE   550 AA;  60690 MW;  5E38B0421C3A1B16 CRC64;

  Query Match             69.1%;  Score 38;  DB 1;  Length 550;
  Best Local Similarity   66.7%;  Pred. No. 4.7;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     417 HHQKLMSNFFAQ 428


RESULT 14
SAS_PIG
ID   SAS_PIG         STANDARD;      PRT;   109 AA.
AC   Q29257;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Sarcoma amplified sequence (Fragment).
GN   SAS.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Small intestine;
RX   MEDLINE=96327607; PubMed=8672129;
RA   Winteroe A.K., Fredholm M., Davies W.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library: analysis of 839 clones.";
RL   Mamm. Genome 7:509-517(1996).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
KW   Glycoprotein; Transmembrane.
FT   DOMAIN        1     12       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     13     33       POTENTIAL.
FT   DOMAIN       34     44       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     45     65       POTENTIAL.
FT   DOMAIN       66     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     73     93       POTENTIAL.
FT   DOMAIN       94   >109       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11291 MW;  5CC5EAB8B7F152B1 CRC64;

  Query Match             65.5%;  Score 36;  DB 1;  Length 109;
  Best Local Similarity   75.0%;  Pred. No. 2.2;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||| |:||
Db      70 HHQVLLFF 77


RESULT 15
TNE6_HUMAN
ID   TNE6_HUMAN      STANDARD;      PRT;   204 AA.
AC   O95857;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tetraspan NET-6.
GN   NET6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Rubinstein E., Serru V., Dessen P., Boucheix C.;
RT   "New tetraspans identified in the EST database.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=20402571; PubMed=10931946;
RA   Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
RA   Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
RA   Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
RA   Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
RA   Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT   "Gene expression profiling in the human hypothalamus-pituitary-adrenal
RT   axis and full-length cDNA cloning.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF120265; AAD17294.1; -.
DR   EMBL; AF100759; AAD43023.1; -.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; FALSE_NEG.
KW   Glycoprotein; Transmembrane.
FT   DOMAIN        1     19       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     20     40       POTENTIAL.
FT   DOMAIN       41     44       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     45     65       POTENTIAL.
FT   DOMAIN       66     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     73     93       POTENTIAL.
FT   DOMAIN       94    167       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    168    188       POTENTIAL.
FT   DOMAIN      189    204       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    137    137       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   204 AA;  22147 MW;  5928646BCD83C0D6 CRC64;
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  Query Match             65.5%;  Score 36;  DB 1;  Length 204;
  Best Local Similarity   75.0%;  Pred. No. 4.2;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFF 8
          ||| |:||
Db     70 HHQVLLFF 77


RESULT 16
SAS_HUMAN
ID   SAS_HUMAN      STANDARD;      PRT;   210 AA.
AC   Q12999; O00577;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Sarcoma amplified sequence.
GN   SAS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Osteosarcoma;
RX   MEDLINE=94181273; PubMed=8134123;
RA   Jankowski S.A., Mitchell D.S., Smith S.H., Trent J.M., Meltzer P.S.;
RT   "SAS, a gene amplified in human sarcomas, encodes a new member of the
RT   transmembrane 4 superfamily of proteins.";
RL   Oncogene 9:1205-1211(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97336055; PubMed=9192850;
RA   Elkahloun A.G., Krizman D.B., Wang Z., Hofmann T.A., Roe B.A.,
RA   Meltzer P.S.;
RT   "Transcript mapping in a 46-kb sequenced region at the core of 12q13.3
RT   amplification in human cancers.";
RL   Genomics 42:295-301(1997).
RN   [3]
RP   REVISIONS TO 76-77 AND 205-210.
RA   Roe B.A.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U01160; AAA17782.1; -.
DR   EMBL; U81031; AAC39524.2; -.
DR   EMBL; BC010377; AAH10377.1; -.
DR   MIM; 181035; -.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
KW   Glycoprotein; Transmembrane.
FT   DOMAIN       1     12       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    13     33       POTENTIAL.
FT   DOMAIN      34     44       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    45     65       POTENTIAL.
FT   DOMAIN      66     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    73     93       POTENTIAL.
FT   DOMAIN      94    173       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   174    194       POTENTIAL.
FT   DOMAIN     195    210       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD   100    100       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   117    117       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   210 AA;  23053 MW;  8A1FF8CC5319755E CRC64;

  Query Match             65.5%;  Score 36;  DB 1;  Length 210;
  Best Local Similarity   75.0%;  Pred. No. 4.3;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFF 8
          ||| |:||
Db     70 HHQVLLFF 77


RESULT 17
G6PI_BUCAI
ID   G6PI_BUCAI     STANDARD;      PRT;   549 AA.
AC   P57636;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN   PGI OR BU573.
OS   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS   symbiotic bacterium).
OC   Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX   NCBI_TaxID=118099;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TOKYO 1998;
RX   MEDLINE=20445173; PubMed=10993077;
RA   Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT   "Genome sequence of the endocellular bacterial symbiont of aphids
RT   Buchnera sp. APS.";
RL   Nature 407:81-86(2000).
CC   -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC       phosphate.
CC   -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AP001119; BAB13263.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW   Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT   ACT_SITE    386    386       BY SIMILARITY.
FT   ACT_SITE    514    514       BY SIMILARITY.
SQ   SEQUENCE   549 AA;  63435 MW;  8DF547CE08382244 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 549;
  Best Local Similarity   58.3%;  Pred. No. 18;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    2;  Gaps    1;

Qy      1 HHQKLV--FFAE 10
          || ||:  |||:
Db    416 HHMKLISNFFAQ 427
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RESULT 18
G6PI_PASMU
ID   G6PI_PASMU     STANDARD;      PRT;   549 AA.
AC   Q9CNL2;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN   PGI OR PM0416.
OS   Pasteurella multocida.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Pasteurella.
OX   NCBI_TaxID=747;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PM70;
RX   MEDLINE=21145866; PubMed=11248100;
RA   May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT   "Complete genomic sequence of Pasteurella multocida Pm70.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC   -!- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE = FRUCTOSE 6-PHOSPHATE.
CC   -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE006077; AAK02500.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW   Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT   ACT_SITE    387    387       BY SIMILARITY.
FT   ACT_SITE    515    515       BY SIMILARITY.
SQ   SEQUENCE   549 AA;  61437 MW;  E6E4856927B93283 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 549;
  Best Local Similarity   58.3%;  Pred. No. 18;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           ||:||:  |||:
Db     417 HHEKLLSNFFAQ 428


RESULT 19
RSG2_HUMAN
ID   RSG2_HUMAN     STANDARD;      PRT;   849 AA.
AC   Q15283; Q15284; O00695; Q99577; Q92594; Q9UEQ2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ras GTPase-activating protein 2 (GAP1m).
GN   RASA2 OR RASGAP OR GAP1M.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97074668; PubMed=8917095;
RA   Kobayashi M., Masui T., Kusuda J., Kameoka Y., Hashimoto K.,
RA   Iwashita S.;
RT   "Human rasGTPase-activating protein (human counterpart of GAP1m):
RT   sequence of the cDNA, primary structure of the protein, production and
RT   chromosomal localization.";
RL   Gene 175:173-177(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97001173; PubMed=8812506;
RA   Li S., Satoh H., Watanabe T., Nakamura S., Hattori S.;
RT   "cDNA cloning and chromosomal mapping of a novel human GAP (GAP1M), a
RT   GTPase-activating protein of Ras.";
RL   Genomics 35:625-627(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=98044291; PubMed=9382842;
RA   Lockyer P.J., Bottomley J.R., Reynolds J.S., McNulty T.J.,
RA   Venkateswarlu K., Potter B.V.L., Dempsey C.E., Cullen P.J.;
RT   "Distinct subcellular localisations of the putative inositol 1,3,4,5-
RT   tetrakisphosphate receptors GAP1(IP4BP) and GAP1m result from the
RT   GAP1(IP4BP) PH domain directing plasma membrane targeting.";
RL   Curr. Biol. 7:1007-1010(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Lockyer P.J.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INHIBITORY REGULATOR OF THE RAS-CYCLIC AMP PATHWAY.
CC       BINDS INOSITOL TETRAKISPHOSPHATE (IP4).
CC   -!- SUBCELLULAR LOCATION: PERINUCLEAR AND CYTOPLASMIC.
CC   -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 BTK DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D78155; BAA11230.1; -.
DR   EMBL; D78156; BAA11231.1; -.
DR   EMBL; D82880; BAA11621.1; -.
DR   EMBL; D82881; BAA11622.1; -.
DR   EMBL; AF115573; AAD09821.1; -.
DR   HSSP; P21707; 1RSY.
DR   MIM; 601589; -.
DR   InterPro; IPR001562; BTK.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR001936; RasGAP.
DR   Pfam; PF00779; BTK; 1.
DR   Pfam; PF00168; C2; 2.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00616; RasGAP; 1.
DR   PRINTS; PR00402; TECBTKDOMAIN.
DR   SMART; SM00107; BTK; 1.
DR   SMART; SM00239; C2; 2.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00323; RasGAP; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
DR   PROSITE; PS50004; C2_DOMAIN_2; 2.
DR   PROSITE; PS00509; RAS_GTPASE_ACTIV_1; FALSE_NEG.
DR   PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
KW   GTPase activation; Repeat.
FT   DOMAIN       25    122       C2 DOMAIN 1.
FT   DOMAIN      166    273       C2 DOMAIN 2.
FT   DOMAIN      356    550       RAS-GAP.
FT   DOMAIN      604    705       PH.
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FT   DOMAIN      707    743       BTK.
FT   DOMAIN        1     26       ALA-RICH.
FT   CONFLICT    216    216       T -> A (IN REF. 1).
FT   CONFLICT    645    645       G -> GS (IN REF. 1).
FT   CONFLICT    645    645       G -> EFIER (IN REF. 2).
SQ   SEQUENCE   849 AA;  96526 MW;  A4B491DFF5C4CB76 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 849;
  Best Local Similarity   77.8%;  Pred. No. 29;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
             || ||| ||
Db     370 HHDKLVPFA 378


RESULT 20
KROS_HUMAN
ID   KROS_HUMAN     STANDARD;      PRT;  2347 AA.
AC   P08922; Q15368;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Proto-oncogene tyrosine-protein kinase ROS precursor (EC 2.7.1.112).
GN   ROS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90280463; PubMed=2352949;
RA   Birchmeier C., O'Neill K., Riggs M., Wigler M.;
RT   "Characterization of ROS1 cDNA from a human glioblastoma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:4799-4803(1990).
RN   [2]
RP   SEQUENCE OF 1790-2259 FROM N.A.
RX   MEDLINE=87064611; PubMed=3023956;
RA   Matsushime H., Wang L.-H., Shibuya M.;
RT   "Human c-ros-1 gene homologous to the v-ros sequence of UR2 sarcoma
RT   virus encodes for a transmembrane receptorlike molecule.";
RL   Mol. Cell. Biol. 6:3000-3004(1986).
RN   [3]
RP   SEQUENCE OF 1854-2245 FROM N.A.
RX   MEDLINE=87064625; PubMed=3785223;
RA   Birchmeier C., Birnbaum D., Waitches G., Fasano O., Wigler M.;
RT   "Characterization of an activated human ros gene.";
RL   Mol. Cell. Biol. 6:3109-3116(1986).
CC   -!- FUNCTION: THIS IS A PROBABLY A CELL GROWTH OR DIFFERENTIATION
CC       FACTOR RECEPTOR WITH A TYROSINE-PROTEIN KINASE ACTIVITY.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC       PROTEIN KINASES. SEVENLESS SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M34353; AAA60278.1; -.
DR   EMBL; M13599; AAA60277.1; -.
DR   EMBL; M13368; AAA60277.1; JOINED.
DR   EMBL; M13591; AAA60277.1; JOINED.
DR   EMBL; M13592; AAA60277.1; JOINED.
DR   EMBL; M13593; AAA60277.1; JOINED.
DR   EMBL; M13594; AAA60277.1; JOINED.
DR   EMBL; M13595; AAA60277.1; JOINED.
DR   EMBL; M13596; AAA60277.1; JOINED.
DR   EMBL; M13597; AAA60277.1; JOINED.
DR   EMBL; M13598; AAA60277.1; JOINED.
DR   EMBL; M13880; AAA36580.1; ALT_TERM.
DR   PIR; A25223; TVHURS.
DR   PIR; A24421; TVHURT.
DR   HSSP; P08631; 1AD5.
DR   MIM; 165020; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR000033; Ldl_receptor_rep.
DR   InterPro; IPR002011; Receptor_tyr_kin_II.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00041; fn3; 7.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00060; FN3; 5.
DR   SMART; SM00135; LY; 2.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
KW   Glycoprotein; ATP-binding; Phosphorylation; Proto-oncogene;
KW   Signal.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28   2347       PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
FT                                ROS.
FT   DOMAIN       28   1859       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1860   1882       POTENTIAL.
FT   DOMAIN     1883   2347       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     1945   2222       PROTEIN KINASE.
FT   NP_BIND    1951   1959       ATP (BY SIMILARITY).
FT   BINDING    1980   1980       ATP (BY SIMILARITY).
FT   MOD_RES    2114   2114       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   CARBOHYD     52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    123    123       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    324    324       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    352    352       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    396    396       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    471    471       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    607    607       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    628    628       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    706    706       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    714    714       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    732    732       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    939    939       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    961    961       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1015   1015       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1087   1087       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1090   1090       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1095   1095       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1211   1211       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1272   1272       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1330   1330       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1458   1458       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1461   1461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1474   1474       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1499   1499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1565   1565       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1669   1669       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1715   1715       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1738   1738       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1808   1808       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   2213   2213       N -> D (IN REF. 2 AND 3).
FT   CONFLICT   2228   2229       QC -> KS (IN REF. 2 AND 3).
FT   CONFLICT   2246   2259       EDGDVICLNSDDIM -> KFDSSEFSSFRCTVN
FT                                (IN REF. 2).
SQ   SEQUENCE   2347 AA;  263956 MW;  E14F3DFD410C1D2A CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 2347;
  Best Local Similarity   55.6%;  Pred. No. 81;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2 HQKLVFFAE 10
           ||:::|:|:|
Db     333 HQQIVYFSE 341


RESULT 21
SLP_BACSU
ID   SLP_BACSU      STANDARD;      PRT;   124 AA.
AC   P39910;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   PAL-related lipoprotein precursor.
GN   SLP OR PAL.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=90368558; PubMed=1697575;
RA   Hemilae H.O., Palva A., Paulin L., Arvidson S., Palva I.;
RT   "Secretory S complex of Bacillus subtilis: sequence analysis and
RT   identity to pyruvate dehydrogenase.";
RL   J. Bacteriol. 172:5052-5063(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=92038903; PubMed=1936936;
RA   Hemilae H.;
RT   "Sequence of a PAL-related lipoprotein from Bacillus subtilis.";
RL   FEMS Microbiol. Lett. 66:37-41(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=97124187; PubMed=8969500;
RA   Winters P., Caldwell R.M., Enfield L., Ferrari E.;
RT   "The ampS-nprE (124 degrees-127 degrees) region of the Bacillus
RT   subtilis 168 chromosome: sequencing of a 27 kb segment and
RT   identification of several genes in the area.";
RL   Microbiology 142:3033-3037(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RA   Caldwell R.M., Ferrari E.;
RT   "Sequence analysis of the mobA-ampS region of the Bacillus subtilis
RT   chromosome.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC       (Probable).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M57435; AAA62685.1; -.
DR   EMBL; AF012285; AAC24936.1; -.
DR   EMBL; Z99111; CAB13335.1; -.
DR   PIR; B54546; B54546.
DR   SubtiList; BG10211; slp.
DR   PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW   Membrane; Lipoprotein; Signal; Complete proteome.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    124       PAL-RELATED LIPOPROTEIN.
FT   LIPID        19     19       N-ACYL DIGLYCERIDE (PROBABLE).
SQ   SEQUENCE   124 AA;  14538 MW;  804401AF0E88446F CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 124;
  Best Local Similarity   40.0%;  Pred. No. 6.3;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           || :::||::
Db      36 HHTQILFFSD 45


RESULT 22
YN51_YEAST
ID   YN51_YEAST     STANDARD;      PRT;   763 AA.
AC   P42843;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 88.9 kDa protein in RFA2-STB1 intergenic region.
GN   YNL311C OR N0376.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / FY1676;
RX   MEDLINE=96076632; PubMed=7502583;
RA   Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.;
RT   "Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV
RT   identifies six known genes, a new member of the hexose transporter
RT   family and ten new open reading frames.";
RL   Yeast 11:1077-1085(1995).
RN   [2]
RP   SEQUENCE OF 149-763 FROM N.A.
RA   Maurer C.T.C., Urbanus J.H.M., Planta R.J.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z46259; CAA86384.1; -.
DR   EMBL; Z71587; CAA96240.1; -.
DR   SGD; S0005255; YNL311C.
DR   InterPro; IPR001810; F-box.
DR   Pfam; PF00646; F-box; 1.
DR   SMART; SM00256; FBOX; 1.
DR   PROSITE; PS50181; FBOX; 1.
KW   Hypothetical protein.
FT   DOMAIN       54    100       F-BOX.
FT   DOMAIN       22     28       POLY-GLU.
SQ   SEQUENCE   763 AA;  88941 MW;  81102168449051BC CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 763;
  Best Local Similarity  100.0%;  Pred. No. 41;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||||
Db     323 HHQKLV 328


RESULT 23
RPOD_PEA
ID   RPOD_PEA       STANDARD;      PRT;  1163 AA.
AC   P12227;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   01-JUL-1993 (Rel. 26, Last annotation update)
```

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DE   DNA-directed RNA polymerase beta" chain (EC 2.7.7.6) (Fragment).
GN   RPOC2.
OS   Pisum sativum (Garden pea).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX   NCBI_TaxID=3888;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86323089; PubMed=3530249;
RA   Cozens A.L., Walker J.E.;
RT   "Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal
RT   subunit S2 and the beta'-subunit of RNA polymerase.";
RL   Biochem. J. 236:453-460(1986).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC       SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03912; CAA27545.1; -.
DR   PIR; S07137; S07137.
DR   Mendel; 5368; PISsa;rpoC2;1.
KW   Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
FT   NON_TER      1     1
SQ   SEQUENCE   1163 AA;  133598 MW;  C92E7BE0A3FDB525 CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 1163;
  Best Local Similarity   66.7%;  Pred. No. 62;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           ||:||: ||
Db    1149 HHRKLLDFA 1157


RESULT 24
ROM2_YEAST
ID   ROM2_YEAST     STANDARD;      PRT;  1356 AA.
AC   P51862;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   RHO1 GDP-GTP exchange protein 2.
GN   ROM2 OR YLR371W OR L8039.3.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA   Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA   Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA   Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA   Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA   Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
RA   Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=96208506; PubMed=8641285;
RA   Ozaki K., Tanaka K., Imamura H., Hihara T., Kameyama T.,
RA   Nonaka H., Hirano H., Matsuura Y., Takai Y.;
RT   "Rom1p and Rom2p are GDP/GTP exchange proteins (GEPs) for the Rholp
RT   small GTP binding protein in Saccharomyces cerevisiae.";
RL   EMBO J. 15:2196-2207(1996).
CC   -!- FUNCTION: STIMULATES THE EXCHANGE OF RHO1 GDP-BOUND FORM INTO
CC       GTP-BOUND FORM.
CC   -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U19103; AAB67564.1; -.
DR   SGD; S0004363; ROM2.
DR   InterPro; IPR001180; CNH.
DR   InterPro; IPR000591; DEP.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00610; DEP; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00036; CNH; 1.
DR   SMART; SM00049; DEP; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS00741; DH_1; FALSE_NEG.
DR   PROSITE; PS50010; DH_2; 1.
KW   Guanine-nucleotide releasing factor.
FT   DOMAIN      659    846       DH.
FT   DOMAIN      252    265       POLY-ASN.
FT   DOMAIN      329    336       POLY-HIS.
FT   DOMAIN      632    635       POLY-ASP.
SQ   SEQUENCE   1356 AA;  152595 MW;  5FBC542114E7BC92 CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 1356;
  Best Local Similarity   50.0%;  Pred. No. 73;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    4;  Gaps    1;

Qy       1 HHQKLV----FFAE 10
             ||::|:    ||||
Db    1131 HHKELINHVSFFAE 1144


RESULT 25
TRX2_HUMAN
ID   TRX2_HUMAN     STANDARD;      PRT;  2715 AA.
AC   Q9UMN6; Q9UK25; O95836; Q9Y669; Q9Y668; O15022;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Trithorax homolog 2 (Mixed lineage leukemia gene homolog 2 protein).
GN   TRX2 OR HRX2 OR MLL2 OR KIAA0340.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RA   Angrand P.O., Valvatne H., Jeanmougin F., Adamson A.,
RA   van der Hoeven F., Olsen L., Tekotte H., Huang N., Poch O.,
RA   Lamerdin J., Chambon P., Losson R., Stewart A., Aasland R.;
RT   "Mammalian trithorax- and ASH1-like proteins: putative chromatin
RT   regulators which contain PHD fingers and SET domains.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RA   Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
RA   Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
RA   Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
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RA   Carrano A.V.;
RT   "Sequence analysis of a 1 Mb region in human 19q13.1.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 816-2715 FROM N.A. (LONG ISOFORM).
RC   TISSUE=Brain;
RX   MEDLINE=97349984; PubMed=9205841;
RA   Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA   Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. VII.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 4:141-150(1997).
RN   [4]
RP   SEQUENCE OF 111-2715 FROM N.A. (LONG ISOFORM).
RC   TISSUE=Testis, and Leukocyte;
RX   MEDLINE=20105772; PubMed=10637508;
RA   Huntsman D.G., Chin S.-F., Muleris M., Batley S.J., Collins V.P.,
RA   Wiedemann L.M., Aparicio S., Caldas C.;
RT   "MLL2, the second human homolog of the Drosophila trithorax gene, maps
RT   to 19q13.1 and is amplified in solid tumor cell lines.";
RL   Oncogene 18:7975-7984(1999).
RN   [5]
RP   PARTIAL SEQUENCE FROM N.A. (LONG AND TRUNCATED ISOFORMS).
RC   TISSUE=Placenta, and Bone marrow;
RX   MEDLINE=99339983; PubMed=10409430;
RA   FitzGerald K.T., Diaz M.O.;
RT   "MLL2: A new mammalian member of the trx/MLL family of genes.";
RL   Genomics 59:187-192(1999).
CC   -!- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       TRUNCATED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVELS IN TESTIS.
CC       ALSO FOUND IN BRAIN, BONE MARROW, HEART, MUSCLE, KIDNEY, PANCREAS,
CC       SPLEEN, THYMUS, PROSTATE, OVARY, INTESTINE, COLON, PERIPHERAL
CC       BLOOD LYMPHOCYTES, AND PLACENTA.
CC   -!- DISEASE: OFTEN AMPLIFIED IN PANCREATIC CARCINOMAS.
CC   -!- SIMILARITY: BELONGS TO THE TRANSCRIPTION FACTOR TRITHORAX FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 SET DOMAIN.
CC   -!- SIMILARITY: CONTAINS 3 PHD-TYPE ZINC FINGERS.
CC   -!- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ007041; CAB45385.1; -.
DR   EMBL; AD000671; -; NOT_ANNOTATED_CDS.
DR   EMBL; AB002302; BAA20763.2; -.
DR   EMBL; AF186605; AAD56420.1; -.
DR   EMBL; AF104918; AAD17932.1; -.
DR   EMBL; AF105279; AAD26113.1; -.
DR   EMBL; AF105280; AAD26112.1; -.
DR   InterPro; IPR000637; AT_hook.
DR   InterPro; IPR003889; FYrich_C.
DR   InterPro; IPR003888; FYrich_N.
DR   InterPro; IPR001965; PHD.
DR   InterPro; IPR003616; PostSET.
DR   InterPro; IPR001214; SET.
DR   InterPro; IPR002857; Znf-CXXC.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00628; PHD; 3.
DR   Pfam; PF00856; SET; 1.
DR   Pfam; PF02008; zf-CXXC; 1.
DR   SMART; SM00384; AT_hook; 1.
DR   SMART; SM00542; FYRC; 1.
DR   SMART; SM00541; FYRN; 1.
DR   SMART; SM00249; PHD; 4.
DR   SMART; SM00508; PostSET; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00317; SET; 1.
DR   PROSITE; PS50280; SET; 1.
KW   DNA-binding; Bromodomain; Nuclear protein; Zinc-finger; Metal-binding;
KW   Transcription regulation; Alternative splicing.
FT   DNA_BIND     37     44       A.T HOOK (BY SIMILARITY).
FT   DNA_BIND    110    117       A.T HOOK (BY SIMILARITY).
FT   DNA_BIND    357    365       A.T HOOK (BY SIMILARITY).
FT   ZN_FING     959   1005       CXXC-TYPE.
FT   ZN_FING    1203   1252       PHD-TYPE 1.
FT   ZN_FING    1253   1303       PHD-TYPE 2.
FT   ZN_FING    1337   1396       PHD-TYPE 3.
FT   DOMAIN     1449   1471       BROMODOMAIN (DIVERGENT).
FT   DOMAIN     2586   2715       SET.
FT   DOMAIN       26     37       POLY-GLY.
FT   DOMAIN      248    255       POLY-PRO.
FT   DOMAIN      362    398       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      402    771       PRO-RICH.
FT   DOMAIN      808    812       POLY-GLN.
FT   DOMAIN     1963   1970       POLY-PRO.
FT   DOMAIN     2251   2259       POLY-PRO.
FT   VARSPLIC    532    582       VSARSSRVIKTPRRFMDEDPPKPPKVEVSPVLRPPITTSPP
FT                                VPQEPAPVPS -> PLSQSLLLPMTLQLSLSLGQWAAPTTS
FT                                ACLDSPLWSPLLLRPRCPLTGLQL (IN ISOFORM
FT                                TRUNCATED).
FT   VARSPLIC    583   2715       MISSING (IN ISOFORM TRUNCATED).
FT   CONFLICT    834    834       K -> E (IN REF. 5).
FT   CONFLICT    941    941       S -> Y (IN REF. 5).
FT   CONFLICT   1317   1317       E -> Q (IN REF. 5).
FT   CONFLICT   1362   1362       H -> Y (IN REF. 5).
FT   CONFLICT   1438   1438       D -> N (IN REF. 5).
FT   CONFLICT   2622   2622       D -> H (IN REF. 5).
SQ   SEQUENCE   2715 AA;  293511 MW;  C0615B981BBEB7BF CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 2715;
  Best Local Similarity   50.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||  ::| ||
Db   .2468 HHDAVIFLAE 2477


RESULT 26
PKSL_BACSU
ID   PKSL_BACSU     STANDARD;      PRT;  4427 AA.
AC   Q05470;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Putative polyketide synthase pksL (PKS).
GN   PKSL OR PKSX OR PKSA OR OUTG.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168 / PB1424;
RX   MEDLINE=93345824; PubMed=8344529;
RA   Scotti C., Piatti M., Cuzzoni A., Perani P., Tognoni A., Grandi G.,
RA   Galizzi A., Albertini A.M.;
RT   "A Bacillus subtilis large ORF coding for a polypeptide highly
RT   similar to polyketide synthases.";
RL   Gene 130:65-71(1993).
RN   [2]
RP   SEQUENCE OF 3619-4427 FROM N.A.
RC   STRAIN=168 / PB1424;
RA   Grandi G.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: POTENTIALLY INVOLVED IN SOME INTERMEDIATE STEPS FOR
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CC       THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN
CC       SECONDARY METABOLISM.
CC   -!- COFACTOR: CONTAINS 5 COVALENTLY BOUND PHOSPHOPANTETHEINES
CC       (POTENTIAL).
CC   -!- SIMILARITY: CONTAINS 5 ACYL CARRIER DOMAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z14098; CAA78479.1; -.
DR   EMBL; U11039; AAA85145.1; -.
DR   EMBL; Z35133; CAA84504.1; -.
DR   EMBL; Z99113; CAB13602.1; -.
DR   PIR; S25021; S25021.
DR   HSSP; P27796; 1PXT.
DR   SubtiList; BG10698; pksL.
DR   InterPro; IPR000794; Ketoacyl-synt.
DR   InterPro; IPR003880; Phosphopant_attach.
DR   Pfam; PF00109; ketoacyl-synt; 4.
DR   Pfam; PF02801; ketoacyl-synt_C; 4.
DR   Pfam; PF00550; pp-binding; 5.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR   PROSITE; PS50075; ACP_DOMAIN; 5.
KW   Transferase; Acyltransferase; Antibiotic biosynthesis; NADP;
KW   Phosphopantetheine; Multifunctional enzyme; Repeat; Complete proteome.
FT   DOMAIN      211    280       ACYL CARRIER (ACP) 1.
FT   DOMAIN      382    759       BETA-KETOACYL SYNTHASE 1.
FT   DOMAIN      937   1115       DEHYDRATASE.
FT   DOMAIN     1409   1602       BETA-KETOACYL REDUCTASE 1.
FT   DOMAIN     1687   1759       ACYL CARRIER (ACP) 2.
FT   DOMAIN     1876   2253       BETA-KETOACYL SYNTHASE 2.
FT   DOMAIN     2491   2560       ACYL CARRIER (ACP) 3.
FT   DOMAIN     2632   2701       ACYL CARRIER (ACP) 4.
FT   DOMAIN     2823   3182       BETA-KETOACYL SYNTHASE 3.
FT   DOMAIN     3575   3776       BETA-KETOACYL REDUCTASE 2.
FT   DOMAIN     3854   3923       ACYL CARRIER (ACP) 5.
FT   DOMAIN     4019   4373       BETA-KETOACYL SYNTHASE 4.
FT   BINDING     243    243       PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING    1723   1723       PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING    2523   2523       PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING    2664   2664       PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING    3886   3886       PHOSPHOPANTETHEINE (POTENTIAL).
SQ   SEQUENCE   4427 AA;  493398 MW;  9612521E561AB9F2 CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 4427;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||||
Db     691 HHQKLV 696


RESULT 27
ACUB_BACSU
ID   ACUB_BACSU     STANDARD;      PRT;   214 AA.
AC   P39066;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetoin utilization acuB protein.
GN   ACUB.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=95020526; PubMed=7934817;
RA   Grundy F.J., Waters D.A., Takova T.Y., Henkin T.M.;
RT   "Identification of genes involved in utilization of acetate and
RT   acetoin in Bacillus subtilis.";
RL   Mol. Microbiol. 10:259-271(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98048467; PubMed=9387221;
RA   Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT   "Sequencing and functional annotation of the Bacillus subtilis genes
RT   in the 200 kb rrnB-dnaB region.";
RL   Microbiology 143:3431-3441(1997).
CC   -!- FUNCTION: ROLE IN GROWTH AND SPORULATION ON ACETOIN OR BUTANEDIOL.
CC       INVOLVED IN THE BREAKDOWN OF THESE COMPOUNDS USED AS A CARBON
CC       SOURCE.
CC   -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L17309; AAA68285.1; -.
DR   EMBL; AF008220; AAC00395.1; -.
DR   EMBL; Z99119; CAB14948.1; -.
DR   PIR; S39644; S39644.
DR   SubtiList; BG10368; acuB.
DR   InterPro; IPR002912; ACT.
DR   InterPro; IPR000644; CBS.
DR   Pfam; PF01842; ACT; 1.
DR   Pfam; PF00571; CBS; 2.
DR   SMART; SM00116; CBS; 2.
KW   Sporulation; Repeat; CBS domain; Complete proteome.
FT   DOMAIN        5     58       CBS 1.
FT   DOMAIN       75    128       CBS 2.
SQ   SEQUENCE   214 AA;  24351 MW;  3B7A964B5C95CCEF CRC64;

  Query Match             60.0%;  Score 33;  DB 1;  Length 214;
  Best Local Similarity   83.3%;  Pred. No. 17;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           |||||:
Db     110 HHQKLI 115


RESULT 28
PPNK_THEMA
ID   PPNK_THEMA     STANDARD;      PRT;   258 AA.
AC   Q9X255;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)
DE   (Poly(P)/ATP NAD kinase).
GN   PPNK OR TM1733.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogales; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
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RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
CC   -!- FUNCTION: Catalyzes the phosphorylation of NAD to NADP. Utilizes
CC       ATP and other nucleoside triphosphates as well as inorganic
CC       polyphosphate as a source of phosphorus (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + NAD(+) = ADP + NADP(+).
CC   -!- COFACTOR: Requires divalent metal ions for activity (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE NAD KINASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001812; AAD36798.1; -.
DR   TIGR; TM1733; -.
DR   InterPro; IPR002504; DUF15.
DR   Pfam; PF01513; DUF15; 1.
KW   Transferase; Kinase; NAD; NADP; Complete proteome.
SQ   SEQUENCE   258 AA;  29241 MW;  45EBBCA0B6FD3EAB CRC64;

  Query Match             60.0%;  Score 33;  DB 1;  Length 258;
  Best Local Similarity   50.0%;  Pred. No. 21;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||  : |||:
Db     140 HHSSMWFFAD 149


RESULT 29
I10S_HUMAN
ID   I10S_HUMAN     STANDARD;      PRT;   325 AA.
AC   Q08334;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE   (Cytokine receptor class-II CRF2-4).
GN   IL10RB OR CRFB4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=93300510; PubMed=8314576;
RA   Lutfalla G., Gardiner K., Uze G.;
RT   "A new member of the cytokine receptor gene family maps on chromosome
RT   21 at less than 35 kb from IFNAR.";
RL   Genomics 16:366-373(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96054036; PubMed=7563119;
RA   Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT   "Structure of the human CRFB4 gene: comparison with its IFNAR
RT   neighbor.";
RL   J. Mol. Evol. 41:338-344(1995).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=97459974; PubMed=9312047;
RA   Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
RA   Pestka S.;
RT   "Identification and functional characterization of a second chain of
RT   the interleukin-10 receptor complex.";
RL   EMBO J. 16:5894-5903(1997).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=20469498; PubMed=10875937;
RA   Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
RA   Wood W.I., Goddard A.D., Gurney A.L.;
RT   "Interleukin (IL)-22, a novel human cytokine that signals through the
RT   interferon receptor-related proteins CRF2-4 and IL-22R.";
RL   J. Biol. Chem. 275:31335-31339(2000).
CC   -!- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY
CC       CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO
CC       INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z17227; CAA78933.1; -.
DR   EMBL; U08988; AAA86872.1; -.
DR   PIR; A47003; A47003.
DR   HSSP; P13726; 1TFH.
DR   MIM; 123889; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_fac.
DR   Pfam; PF01108; Tissue_fac; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    325       INTERLEUKIN-10 RECEPTOR BETA CHAIN.
FT   DOMAIN      20    220       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   221    242       POTENTIAL.
FT   DOMAIN     243    325       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     113    205       FIBRONECTIN TYPE-III.
FT   DISULFID    66     74       BY SIMILARITY.
FT   DISULFID   188    209       BY SIMILARITY.
FT   CARBOHYD    49     49       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   124    124       A -> D (IN REF. 2).
FT   CONFLICT   269    273       FLGHP -> VGRME (IN REF. 2).
FT   CONFLICT   274    325       MISSING (IN REF. 2).
SQ   SEQUENCE   325 AA;  37011 MW;  66706C79F8514B23 CRC64;

  Query Match             60.0%;  Score 33;  DB 1;  Length 325;
  Best Local Similarity   55.6%;  Pred. No. 27;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           ||  |:||:
Db     274 HHNTLLFFS 282


RESULT 30
C7D9_SOYBN
ID   C7D9_SOYBN     STANDARD;      PRT;   496 AA.
AC   O81971;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Cytochrome P450 71D9 (EC 1.14.-.-) (P450 CP3).
GN   CYP71D9.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. HAROSOY 63;
RX   MEDLINE=98311068; PubMed=9648734;
RA   Schopfer C.R., Ebel J.;
RT   "Identification of elicitor-induced cytochrome P450s of soybean
RT   (Glycine max L.) using differential display of mRNA.";
RL   Mol. Gen. Genet. 258:315-322(1998).
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Y10490; CAA71514.1; -.
DR   InterPro; IPR001128; Cyt_P450.
DR   Pfam; PF00067; p450; 1.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Oxidoreductase; Monooxygenase; Heme.
FT   BINDING     437    437       HEME (BY SIMILARITY).
SQ   SEQUENCE   496 AA;  56205 MW;  9C90947C8A546CE1 CRC64;

  Query Match             60.0%;  Score 33;  DB 1;  Length 496;
  Best Local Similarity   83.3%;  Pred. No. 41;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           |||||:
Db     197 HHQKLI 202


RESULT 31
G6PI_HAEIN
ID   G6PI_HAEIN     STANDARD;      PRT;   549 AA.
AC   P44312;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN   PGI OR HI1576.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RD / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus
RT   influenzae Rd.";
RL   Science 269:496-512(1995).
CC   -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC       phosphate.
CC   -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U32831; AAC23219.1; ALT_INIT.
DR   TIGR; HI1576; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW   Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT   ACT_SITE    387    387       BY SIMILARITY.
FT   ACT_SITE    515    515       BY SIMILARITY.
SQ   SEQUENCE   549 AA;  61622 MW;  F65348C667068F16 CRC64;

  Query Match             60.0%;  Score 33;  DB 1;  Length 549;
  Best Local Similarity   58.3%;  Pred. No. 46;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           || ||:  |||:
Db     417 HHNKLLSNFFAQ 428


RESULT 32
SYT_MYCGE
ID   SYT_MYCGE      STANDARD;      PRT;   564 AA.
AC   P47615;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
DE   (ThrRS).
GN   THRS OR MG375.
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC   Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=96026346; PubMed=7569993;
RA   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA   Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403(1995).
RN   [2]
RP   SEQUENCE OF 350-463 FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=94075230; PubMed=8253680;
RA   Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT   "A survey of the Mycoplasma genitalium genome by using random
RT   sequencing.";
RL   J. Bacteriol. 175:7918-7930(1993).
CC   -!- CATALYTIC ACTIVITY: ATP + L-threonine + tRNA(Thr) = AMP +
CC       diphosphate + L-threonyl-tRNA(Thr).
CC   -!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U39719; AAC71602.1; -.
DR   EMBL; U02130; AAD12408.1; -.
DR   HSSP; P00955; 1EVL.
DR   TIGR; MG375; -.
DR   InterPro; IPR002106; AA_tRNA_ligase_II.
DR   InterPro; IPR004154; HGTP_anticodon.
DR   InterPro; IPR002314; tRNA-synt_2b.
DR   InterPro; IPR002320; tRNA-synt_thr.
DR   Pfam; PF03129; HGTP_anticodon; 1.
DR   Pfam; PF00587; tRNA-synt_2b; 1.
DR   PRINTS; PR01047; TRNASYNTHTHR.
DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Metal-binding; Zinc; Complete proteome.
FT   DOMAIN      167    464       CATALYTIC.
FT   METAL       260    260       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       311    311       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       441    441       ZINC (CATALYTIC) (BY SIMILARITY).
SQ   SEQUENCE   564 AA;  65595 MW;  2CA833DA7F7AC447 CRC64;

  Query Match             60.0%;  Score 33;  DB 1;  Length 564;
  Best Local Similarity   71.4%;  Pred. No. 47;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVF 7
           |||:|:|
Db     207 HHQQLLF 213


RESULT 33
SDC3_CAEEL
ID   SDC3_CAEEL     STANDARD;      PRT;  2150 AA.
AC   P34706;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Zinc finger protein sdc-3.
GN   SDC-3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=93161411; PubMed=8431944;
RA   Klein R.D., Meyer B.J.;
RT   "Independent domains of the Sdc-3 protein control sex determination
RT   and dosage compensation in C. elegans.";
RL   Cell 72:349-364(1993).
CC   -!- FUNCTION: CONTROLS BOTH SEX DETERMINATION AND X CHROMOSOME DOSAGE
CC       COMPENSATION. THESE TWO FUNCTIONS ACT INDEPENDENTLY.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYONIC AND EARLY LARVAL
CC       STAGES.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M85149; AAA28144.1; -.
DR   PIR; S27802; S27802.
DR   InterPro; IPR000822; Znf-C2H2.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; FALSE_NEG.
KW   Developmental protein; Zinc-finger; Metal-binding; DNA-binding;
KW   Nuclear protein; Repeat.
FT   DOMAIN      443    987       DOSAGE COMPENSATION DOMAIN 1.
FT   DOMAIN     1508   1516       SEX DETERMINATION DOMAIN.
FT   DOMAIN     2080   2105       DOSAGE COMPENSATION DOMAIN 2.
FT   ZN_FING    2078   2105       C2H2-TYPE.
FT   ZN_FING    2117   2141       C2H2-TYPE.
SQ   SEQUENCE  2150 AA;  249954 MW;  7430D77AC784EA46 CRC64;

  Query Match             60.0%;  Score 33;  DB 1;  Length 2150;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           || :  |||:
Db    2140 HHSRRCFFAD 2149


RESULT 34
G6PI_KLEOX
ID   G6PI_KLEOX     STANDARD;      PRT;  167 AA.
AC   P77877;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Fragment).
GN   PGI.
OS   Klebsiella oxytoca.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Klebsiella.
OX   NCBI_TaxID=571;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EA321;
RX   MEDLINE=97032593; PubMed=8875859;
RA   Katz L.A.;
RT   "Transkingdom transfer of the phosphoglucose isomerase gene.";
RL   J. Mol. Evol. 43:453-459(1996).
CC   -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC       phosphate.
CC   -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U54763; AAB50058.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; PARTIAL.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; PARTIAL.
KW   Isomerase; Gluconeogenesis; Glycolysis.
FT   NON_TER       1      1
FT   NON_TER     167    167
SQ   SEQUENCE   167 AA;  18875 MW;  F6C56A969F06F891 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 167;
  Best Local Similarity   58.3%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           || ||:  |||:
Db     115 HHPKLLSNFFAQ 126


RESULT 35
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CALC_MOUSE
ID   CALC_MOUSE     STANDARD;      PRT;   178 AA.
AC   Q63811;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calcineurin B subunit isoform 2 (Protein phosphatase 2B regulatory
DE   subunit 2) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE   2).
GN   PPP3R2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92392379; PubMed=1325794;
RA   Ueki K., Muramatsu T., Kincaid R.L.;
RT   "Structure and expression of two isoforms of the murine calmodulin-
RT   dependent protein phosphatase regulatory subunit (calcineurin B).";
RL   Biochem. Biophys. Res. Commun. 187:537-543(1992).
CC   -!- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIM, A CALCIUM-DEPENDENT,
CC       CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC       SENSITIVITY.
CC   -!- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC       SUBUNIT (B).
CC   -!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S43865; AAB23172.1; -.
DR   HSSP; P06705; 1TCO.
DR   MGD; MGI:107171; Ppp3r2.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Myristate.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   LIPID         1      1       MYRISTATE (BY SIMILARITY).
FT   CA_BIND      30     41       EF-HAND 1.
FT   CA_BIND      62     73       EF-HAND 2.
FT   CA_BIND      99    110       EF-HAND 3.
FT   CA_BIND     140    151       EF-HAND 4.
SQ   SEQUENCE   178 AA;  20528 MW;  F453B9A047C240F5 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 178;
  Best Local Similarity   66.7%;  Pred. No. 23;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           |:||| | |
Db     162 HKKLVVFVE 170


RESULT 36
CYF_GUITH
ID   CYF_GUITH      STANDARD;      PRT;   321 AA.
AC   O78494;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apocytochrome F precursor.
GN   PETA.
OS   Guillardia theta (Cryptomonas phi).
OG   Chloroplast.
OC   Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX   NCBI_TaxID=55529;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99128221; PubMed=9929392;
RA   Douglas S.E., Penny S.L.;
RT   "The plastid genome of the cryptophyte alga, Guillardia theta:
RT   complete sequence and conserved synteny groups confirm its common
RT   ancestry with red algae.";
RL   J. Mol. Evol. 48:236-244(1999).
CC   -!- FUNCTION: TRANSLOCATES PROTONS ACROSS THE THYLAKOID MEMBRANE AND
CC       TRANSFERS ELECTRONS FROM PHOTOSYSTEM II TO PHOTOSYSTEM I. IT
CC       RECEIVES ELECTRONS FROM THE RIESKE IRON-SULFUR PROTEIN AND PASSES
CC       THEM TO PLASTOCYANIN; THIS FUNCTION IS VERY SIMILAR TO THAT OF
CC       MITOCHONDRIAL CYTOCHROME C1.
CC   -!- SUBUNIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING
CC       CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN.
CC   -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane (Probable).
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF041468; AAC35685.1; -.
DR   HSSP; P36438; 1HCZ.
DR   InterPro; IPR002325; Apocyt_F.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   Pfam; PF01333; Apocytochrome_F; 1.
DR   PRINTS; PR00610; CYTOCHROMEF.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
KW   Electron transport; Heme; Chloroplast; Thylakoid;
KW   Photosynthesis; Photosystem I; Photosystem II; Transit peptide;
KW   Transmembrane.
FT   TRANSIT       1     38       CHLOROPLAST (BY SIMILARITY).
FT   CHAIN        39    321       APOCYTOCHROME F.
FT   BINDING      59     59       HEME (COVALENT) (PROBABLE).
FT   BINDING      62     62       HEME (COVALENT) (PROBABLE).
FT   METAL        63     63       IRON (HEME AXIAL LIGAND) (PROBABLE).
FT   TRANSMEM    287    307       POTENTIAL.
SQ   SEQUENCE   321 AA;  35173 MW;  42A1FF89FB05AE3D CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVF 7
             ||||||
Db     161 HQKLVF 166


RESULT 37
FD3E_SOYBN
ID   FD3E_SOYBN     STANDARD;      PRT;   380 AA.
AC   P48625;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-).
GN   FAD3.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Seed;
RX   MEDLINE=94302147; PubMed=8029334;
RA   Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
RA   Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,
RA   Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA   Feldmann K.A., Pierce J., Browse J.;
RT   "Cloning of higher plant omega-3 fatty acid desaturases.";
RL   Plant Physiol. 103:467-476(1993).
CC   -!- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC       THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC       IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC       CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC       ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC       PHOSPHOLIPIDS.
CC   -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC   -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC       AND/ OR BE INVOLVED IN METAL ION BINDING.
CC   -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L22964; AAA61777.1; -.
DR   PIR; JQ2338; JQ2338.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 1.
KW   Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW   Transmembrane.
FT   TRANSMEM     55     75       POTENTIAL.
FT   TRANSMEM    212    232       POTENTIAL.
FT   TRANSMEM    236    256       POTENTIAL.
FT   DOMAIN      100    104       HISTIDINE BOX 1.
FT   DOMAIN      136    140       HISTIDINE BOX 2.
FT   DOMAIN      303    307       HISTIDINE BOX 3.
SQ   SEQUENCE   380 AA;  44185 MW;  BF800F93CF4C29D7 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 380;
  Best Local Similarity   62.5%;  Pred. No. 50;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||||| ::
Db     264 HHQKLPWY 271


RESULT 38
LBP_HUMAN
ID   LBP_HUMAN      STANDARD;      PRT;   481 AA.
AC   P18428; Q92672; O43438; Q9UD66; Q9H403;
DT   01-NOV-1990 (Rel. 16, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Lipopolysaccharide-binding protein precursor (LBP).
GN   LBP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90385281; PubMed=2402637;
RA   Schumann R.R., Leong S.R., Flaggs G.W., Gray P.W., Wright S.D.,
RA   Mathison J.C., Tobias P.S., Ulevitch R.J.;
RT   "Structure and function of lipopolysaccharide binding protein.";
RL   Science 249:1429-1431(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94292492; PubMed=7517398;
RA   Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
RA   Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
RT   "Bactericidal/permeability-increasing protein and lipopolysaccharide
RT   (LPS)-binding protein. LPS binding properties and effects on LPS-
RT   mediated cell activation.";
RL   J. Biol. Chem. 269:17411-17416(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Hubacek J.A., Aslanidis C., Schmitz G.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98110577; PubMed=9441745;
RA   Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D.,
RA   Seilhamer J.J., Schumann R.R.;
RT   "Similar organization of the lipopolysaccharide-binding protein (LBP)
RT   and phospholipid transfer protein (PLTP) genes suggests a common gene
RT   family of lipid-binding proteins.";
RL   Genomics 46:416-425(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;
RT   "Cloning and sequencing of human lipopolysaccharide-binding protein
RT   gene.";
RL   Sheng Wu Huaxue Yu Shengwu Wuli Jinzhan 25:469-471(1998).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [7]
RP   SEQUENCE OF 1-41 FROM N.A.
RA   Sutton C.L., Smith R.I.F., Centola M.B., Theofan G.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=98227852; PubMed=9568897;
RA   Beamer L.J.; Carroll S.F., Eisenberg D.;
RT   "The BPI/LBP family of proteins: a structural analysis of conserved
RT   regions.";
RL   Protein Sci. 7:906-914(1998).
CC   -!- FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL
CC       LIPOPOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE OUTER
CC       MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS
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CC       TO INTERACT WITH THE CD14 RECEPTOR.
CC   -!- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M35533; AAA59493.1; -.
DR   EMBL; X98657; CAA67226.1; -.
DR   EMBL; X98658; CAA67226.1; JOINED.
DR   EMBL; X98659; CAA67226.1; JOINED.
DR   EMBL; X98660; CAA67226.1; JOINED.
DR   EMBL; X98661; CAA67226.1; JOINED.
DR   EMBL; X98662; CAA67226.1; JOINED.
DR   EMBL; X98663; CAA67226.1; JOINED.
DR   EMBL; X98664; CAA67226.1; JOINED.
DR   EMBL; X98665; CAA67226.1; JOINED.
DR   EMBL; X98666; CAA67226.1; JOINED.
DR   EMBL; X98667; CAA67226.1; JOINED.
DR   EMBL; X98668; CAA67226.1; JOINED.
DR   EMBL; AF013512; AAC39547.1; -.
DR   EMBL; AF013500; AAC39547.1; JOINED.
DR   EMBL; AF013501; AAC39547.1; JOINED.
DR   EMBL; AF013502; AAC39547.1; JOINED.
DR   EMBL; AF013503; AAC39547.1; JOINED.
DR   EMBL; AF013504; AAC39547.1; JOINED.
DR   EMBL; AF013505; AAC39547.1; JOINED.
DR   EMBL; AF013506; AAC39547.1; JOINED.
DR   EMBL; AF013507; AAC39547.1; JOINED.
DR   EMBL; AF013508; AAC39547.1; JOINED.
DR   EMBL; AF013509; AAC39547.1; JOINED.
DR   EMBL; AF013510; AAC39547.1; JOINED.
DR   EMBL; AF013511; AAC39547.1; JOINED.
DR   EMBL; AF105067; AAD21962.1; -.
DR   EMBL; AL080249; CAC10462.1; -.
DR   EMBL; L42172; AAA66446.1; -.
DR   PIR; A35843; A35843.
DR   HSSP; P17213; 1BP1.
DR   MIM; 151990; -.
DR   InterPro; IPR001124; LBP_BPI_CETP.
DR   Pfam; PF01273; LBP_BPI_CETP; 1.
DR   Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR   SMART; SM00328; BPI1; 1.
DR   SMART; SM00329; BPI2; 1.
DR   PROSITE; PS00400; LBP_BPI_CETP; 1.
KW   Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     25
FT   CHAIN       26    481       LIPOPOLYSACCHARIDE-BINDING PROTEIN.
FT   CARBOHYD    300    300       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    355    355       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    386    386       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    394    394       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      6      6       R -> H (IN REF. 2).
FT   CONFLICT     22     22       E -> C (IN REF. 2).
FT   CONFLICT     82     82       N -> K (IN REF. 4).
FT   CONFLICT    128    128       S -> F (IN REF. 4).
FT   CONFLICT    154    157       VTAS -> GYCL (IN REF. 1).
FT   CONFLICT    174    174       L -> S (IN REF. 1).
FT   CONFLICT    257    257       R -> S (IN REF. 4).
FT   CONFLICT    266    270       VMSLP -> A (IN REF. 1).
FT   CONFLICT    369    369       L -> H (IN REF. 4).
FT   CONFLICT    436    436       L -> F (IN REF. 2, 4 AND 6).
SQ   SEQUENCE   481 AA;  53349 MW;  816E4B9E5E6864D0 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 481;
  Best Local Similarity   62.5%;  Pred. No. 63;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFA 9
           | |:|:||
Db     273 HNKMVYFA 280


RESULT 39
CPBJ_MOUSE
ID   CPBJ_MOUSE     STANDARD;      PRT;   492 AA.
AC   O55071;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Cytochrome P450 2B19 (EC 1.14.14.1) (CYPIIB19).
GN   CYP2B19.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Skin;
RX   MEDLINE=99017986; PubMed=9799616;
RA   Keeney D.S.;
RT   "The novel skin-specific cytochrome P450 Cyp2b19 maps to proximal
RT   chromosome 7 in the mouse, near a cluster of Cyp2 family genes.";
RL   Genomics 53:417-419(1998).
CC   -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC       MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC       NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC       OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC       ACIDS, AND XENOBIOTICS.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN DIFFERENTIATED KERATINOCYTES
CC       IN SKIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF047529; AAC78770.1; -.
DR   HSSP; P00179; 1DT6.
DR   MGD; MGI:107303; Cyp2b19.
DR   InterPro; IPR001128; Cyt_P450.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum; Phosphorylation.
FT   MOD_RES     129    129       PHOSPHORYLATION (BY CAPK) (BY
FT                                SIMILARITY).
FT   BINDING     437    437       HEME (BY SIMILARITY).
SQ   SEQUENCE   492 AA;  55996 MW;  9E685AF61EE2DFA2 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 492;
  Best Local Similarity   53.3%;  Pred. No. 65;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    6;  Gaps    1;

Qy       1 HHQKLV------FFA 9
           ||| ||      |||
Db     285 HHQNLVISVLSLFFA 299


RESULT 40
MURC_RICPR
ID   MURC_RICPR     STANDARD;      PRT;   495 AA.
AC   Q9ZDS8;
DT   30-MAY-2000 (Rel. 39, Created)
```

```
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8) (UDP-N-
DE   acetylmuramoyl-L-alanine synthetase).
GN   MURC OR RP247.
OS   Rickettsia prowazekii.
OC   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia.
OX   NCBI_TaxID=782;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MADRID E;
RX   MEDLINE=99039499; PubMed=9823893;
RA   Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA   Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA   Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT   "The genome sequence of Rickettsia prowazekii and the origin of
RT   mitochondria.";
RL   Nature 396:133-140(1998).
CC   -!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP +
CC       phosphate + UDP-N-acetylmuramoyl-L-alanine.
CC   -!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ235271; CAA14709.1; -.
DR   InterPro; IPR000713; Mur_ligase.
DR   InterPro; IPR004101; Mur_ligase_C.
DR   Pfam; PF01225; Mur_ligase; 1.
DR   Pfam; PF02875; Mur_ligase_C; 1.
KW   Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
KW   ATP-binding; Complete proteome.
FT   NP_BIND     120    126       ATP (POTENTIAL).
SQ   SEQUENCE   495 AA;  54612 MW;  2E18464088FAD2D6 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 495;
  Best Local Similarity   60.0%;  Pred. No. 65;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           || |  | ||
Db     428 HHDKANFLAE 437


RESULT 41
ACHB_MOUSE
ID   ACHB_MOUSE     STANDARD;      PRT;   501 AA.
AC   P09690;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholine receptor protein, beta chain precursor.
GN   CHRNB1 OR ACRB.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87057335; PubMed=3782129;
RA   Buonanno A., Mudd J., Shah V., Merlie J.P.;
RT   "A universal oligonucleotide probe for acetylcholine receptor genes.
RT   Selection and sequencing of cDNA clones for the mouse muscle beta
RT   subunit.";
RL   J. Biol. Chem. 261:16451-16458(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89214211; PubMed=2708381;
RA   Buonanno A., Mudd J., Merlie J.P.;
RT   "Isolation and characterization of the beta and epsilon subunit genes
RT   of mouse muscle acetylcholine receptor.";
RL   J. Biol. Chem. 264:7611-7616(1989).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M14537; AAA37154.1; -.
DR   EMBL; J04699; AAA37156.1; -.
DR   PIR; A25338; A25338.
DR   MGD; MGI:87890; Chrnb1.
DR   InterPro; IPR000188; GABAA_receptor.
DR   InterPro; IPR001175; Neur_channel.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Phosphorylation.
FT   SIGNAL       1     23
FT   CHAIN       24    501       ACETYLCHOLINE RECEPTOR PROTEIN, BETA
FT                               CHAIN.
FT   DOMAIN      24    244       EXTRACELLULAR.
FT   TRANSMEM   245    269
FT   TRANSMEM   277    295
FT   TRANSMEM   311    332
FT   DOMAIN     333    469       CYTOPLASMIC.
FT   TRANSMEM   470    488
FT   DISULFID   151    165       BY SIMILARITY.
FT   CARBOHYD   164    164       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   MOD_RES    390    390       PHOSPHORYLATION (BY TYR-KINASES)
FT                               (BY SIMILARITY).
SQ   SEQUENCE   501 AA;  56930 MW;  787BDDA90EBB0EF2 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 501;
  Best Local Similarity   37.5%;  Pred. No. 66;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||:::|:
Db     231 HHEEVIFY 238


RESULT 42
ACHG_HUMAN
ID   ACHG_HUMAN     STANDARD;      PRT;   517 AA.
AC   P07510;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholine receptor protein, gamma chain precursor.
GN   CHRNG OR ACHRG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85101368; PubMed=3967651;
RA   Shibahara S., Kubo T., Perski H.J., Takahashi H., Noda M., Numa S.;
RT   "Cloning and sequence analysis of human genomic DNA encoding gamma
RT   subunit precursor of muscle acetylcholine receptor.";
RL   Eur. J. Biochem. 146:15-22(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle fibroblast;
RX   MEDLINE=93345508; PubMed=7688301;
RA   Beeson D.M.W., Brydson M., Betty M., Jeremiah S., Povey S.,
RA   Vincent A., Newsom-Davis J.;
RT   "Primary structure of the human muscle acetylcholine receptor. cDNA
RT   cloning of the gamma and epsilon subunits.";
RL   Eur. J. Biochem. 215:229-238(1993).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M11811; AAA51568.2; -.
DR   EMBL; L29197; AAA51568.2; JOINED.
DR   EMBL; X01715; CAA25861.1; ALT_SEQ.
DR   EMBL; X01716; CAA25861.1; JOINED.
DR   EMBL; X01717; CAA25861.1; JOINED.
DR   EMBL; X01718; CAA25861.1; JOINED.
DR   EMBL; X01719; CAA25861.1; JOINED.
DR   EMBL; X01720; CAA25861.1; JOINED.
DR   EMBL; X01721; CAA25861.1; JOINED.
DR   EMBL; X04759; CAA25861.1; JOINED.
DR   PIR; A23261; A23261.
DR   PIR; S34776; S34776.
DR   MIM; 100730; -.
DR   InterPro; IPR000188; GABAA_receptor.
DR   InterPro; IPR001175; Neur_channel.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL       1     22
FT   CHAIN       23    517       ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA
FT                               CHAIN.
FT   DOMAIN      23    240       EXTRACELLULAR.
FT   TRANSMEM   241    265
FT   TRANSMEM   275    293
FT   TRANSMEM   309    330
FT   DOMAIN     331    474       CYTOPLASMIC.
FT   TRANSMEM   475    495
FT   DISULFID   150    164       BY SIMILARITY.
FT   CARBOHYD    52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   517 AA;  57897 MW;  D4587257087E102C CRC64;

  Query Match           58.2%;  Score 32;  DB 1;  Length 517;
  Best Local Similarity  71.4%;  Pred. No. 68;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFF 8
           |||:||:
Db     228 HQKVVFY 234


RESULT 43
ACHG_BOVIN
ID   ACHG_BOVIN     STANDARD;      PRT;   519 AA.
AC   P13536;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Acetylcholine receptor protein, gamma chain precursor.
GN   CHRNG.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84285374; PubMed=6547904;
RA   Takai T., Noda M., Furutani Y., Takahashi H., Notake M., Shimizu S.,
RA   Kayano T., Tanabe T., Tanaka K.-I., Hirose T., Inayama S., Numa S.;
RT   "Primary structure of gamma subunit precursor of calf-muscle
RT   acetylcholine receptor deduced from the cDNA sequence.";
RL   Eur. J. Biochem. 143:109-115(1984).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M28307; AAA30351.1; -.
DR   InterPro; IPR000188; GABAA_receptor.
DR   InterPro; IPR001175; Neur_channel.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL       1     22
FT   CHAIN       23    519       ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA
FT                               CHAIN.
FT   DOMAIN      23    240       EXTRACELLULAR.
FT   TRANSMEM   241    265
FT   TRANSMEM   274    292
FT   TRANSMEM   308    329
FT   DOMAIN     330    476       CYTOPLASMIC.
FT   TRANSMEM   477    497
FT   DISULFID   150    164       BY SIMILARITY.
FT   CARBOHYD    52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   519 AA;  58178 MW;  B72DE5487F7B5C4E CRC64;

  Query Match           58.2%;  Score 32;  DB 1;  Length 519;
  Best Local Similarity  71.4%;  Pred. No. 68;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2 HQKLVFF 8
            |||:||:
Db     228 HQKVVFY 234


RESULT 44
ACHG_MOUSE
ID   ACHG_MOUSE     STANDARD;      PRT;   519 AA.
AC   P04760;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholine receptor protein, gamma chain precursor.
GN   CHRNG OR ACRG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86205253; PubMed=3010242;
RA   Yu L., Lapolla R.J., Davidson N.;
RT   "Mouse muscle nicotinic acetylcholine receptor gamma subunit: cDNA
RT   sequence and gene expression.";
RL   Nucleic Acids Res. 14:3539-3555(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86308110; PubMed=3755765;
RA   Boulter J., Evans K., Martin G., Mason P., Stengelin S.,
RA   Goldman D.J., Heinemann S.F., Patrick J.;
RT   "Isolation and sequence of cDNA clones coding for the precursor to
RT   the gamma subunit of mouse muscle nicotinic acetylcholine receptor.";
RL   J. Neurosci. Res. 16:37-49(1986).
RN   [3]
RP   SEQUENCE OF 1-57 FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=88108850; PubMed=3480767;
RA   Gardner P.D., Heinemann S.F., Patrick J.;
RT   "Transcriptional regulation of nicotinic acetylcholine receptor
RT   genes: identification of control elements of a gamma-subunit gene.";
RL   Brain Res. 427:69-76(1987).
RN   [4]
RP   SEQUENCE OF 1-18 FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=89218986; PubMed=3244354;
RA   Crowder C.M., Merlie J.P.;
RT   "Stepwise activation of the mouse acetylcholine receptor delta- and
RT   gamma-subunit genes in clonal cell lines.";
RL   Mol. Cell. Biol. 8:5257-5267(1988).
RN   [5]
RP   SEQUENCE OF 115-170 FROM N.A. (LONG AND SHORT FORMS).
RX   MEDLINE=95224005; PubMed=7708706;
RA   Mileo A.M., Monaco L., Palma E., Grassi F., Miledi R., Eusebi F.;
RT   "Two forms of acetylcholine receptor gamma subunit in mouse muscle.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:2686-2690(1995).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: AT LEAST IN MYOTUBES OF SKELETAL MUSCLE.
CC   -!- DEVELOPMENTAL STAGE: BOTH SHORT AND LONG ISOFORMS ARE FOUND IN A
CC       17 DAYS OLD EMBRYO, WHEREAS THE SHORT VARIANT IS THE ONLY ISOFORM
CC       PRESENT IN THE NEWBORN MUSCLE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X03818; CAA27442.1; -.
DR   EMBL; X03819; CAA27443.1; -.
DR   EMBL; M30514; AAB63431.1; ALT_SEQ.
DR   EMBL; M27455; AAA70247.1; -.
DR   EMBL; M22381; AAA37152.1; -.
DR   EMBL; S77465; AAB33997.2; -.
DR   PIR; A24919; A24919.
DR   MGD; MGI:87895; Chrng.
DR   InterPro; IPR000188; GABAA_receptor.
DR   InterPro; IPR001175; Neur_channel.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Alternative splicing.
FT   SIGNAL        1     22
FT   CHAIN        23    519       ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA
FT                                 CHAIN.
FT   DOMAIN        23    240       EXTRACELLULAR.
FT   TRANSMEM     241    265
FT   TRANSMEM     274    292
FT   TRANSMEM     308    329
FT   DOMAIN       330    476       CYTOPLASMIC.
FT   TRANSMEM     477    497
FT   DISULFID     150    164       BY SIMILARITY.
FT   CARBOHYD      52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     163    163       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   VARSPLIC     117    168       MISSING (IN SHORT ISOFORM).
FT   CONFLICT     231    231       V -> G (IN REF. 2).
FT   CONFLICT     346    346       L -> V (IN REF. 2).
SQ   SEQUENCE   519 AA;  58745 MW;  3F435303564C8048 CRC64;

  Query Match           58.2%;  Score 32;  DB 1;  Length 519;
  Best Local Similarity  71.4%;  Pred. No. 68;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFF 8
            |||:||:
Db     228 HQKVVFY 234


RESULT 45
ACHG_RAT
ID   ACHG_RAT       STANDARD;      PRT;   519 AA.
AC   P18916;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Acetylcholine receptor protein, gamma chain precursor.
GN   CHRNG OR ACHRG.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=91099317; PubMed=1702709;
RA   Witzemann V., Stein E., Barg B., Konno T., Koenen M., Kues W.,
RA   Criado M., Hofmann M., Sakmann B.;
RT   "Primary structure and functional expression of the alpha-, beta-,
RT   gamma-, delta- and epsilon-subunits of the acetylcholine receptor
RT   from rat muscle.";
RL   Eur. J. Biochem. 194:437-448(1990).
RN   [2]
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RP   SEQUENCE OF 203-306 FROM N.A.
RX   MEDLINE=88030021; PubMed=3666131;
RA   Witzemann V., Barg B., Nishikawa Y., Sakmann B., Numa S.;
RT   "Differential regulation of muscle acetylcholine receptor gamma- and
RT   epsilon-subunit mRNAs.";
RL   FEBS Lett. 223:104-112(1987).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X74834; CAA52828.1; -.
DR   EMBL; X06364; CAA29662.1; -.
DR   PIR; S03082; S03082.
DR   PIR; S13874; S13874.
DR   InterPro; IPR000188; GABAA_receptor.
DR   InterPro; IPR001175; Neur_channel.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    519       ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA
FT                               CHAIN.
FT   DOMAIN      23    240       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   241    265       POTENTIAL.
FT   TRANSMEM   274    292       POTENTIAL.
FT   TRANSMEM   308    329       POTENTIAL.
FT   DOMAIN     330    476       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   477    497       POTENTIAL.
FT   DISULFID   150    164       BY SIMILARITY.
FT   CARBOHYD    52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   519 AA;  58621 MW;  1C97A83DE42A0D09 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 519;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQKLVFF 8
          |||:||:
Db    228 HQKVVFY 234


RESULT 46
PRXV_ASCNO
ID   PRXV_ASCNO     STANDARD;      PRT;   557 AA.
AC   P81701;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Vanadium haloperoxidase (EC 1.11.1.-) (V-BPO).
OS   Ascophyllum nodosum.
OC   Eukaryota; stramenopiles; Phaeophyceae; Fucales; Fucaceae;
OC   Ascophyllum.
OX   NCBI_TaxID=52969;
RN   [1]
RP   SEQUENCE, X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND FUNCTION.
RX   MEDLINE=20013071; PubMed=10543953;
RA   Weyand M., Hecht H.-J., Kiess M., Liaud M.-F., Vilter H.,
RA   Schomburg D.;
RT   "X-ray structure determination of a vanadium-dependent
RT   haloperoxidase from Ascophyllum nodosum at 2.0-A resolution.";
RL   J. Mol. Biol. 293:595-611(1999).
RN   [2]
RP   SEQUENCE OF 320-556 FROM N.A., SEQUENCE OF 326-341; 383-426; 471-479
RP   AND 481-556, AND FUNCTION.
RX   MEDLINE=96081028; PubMed=8564812;
RA   Vilter H.;
RT   "Vanadium-dependent haloperoxidases.";
RL   (In) Sigel H., Sigel A. (eds.);
RL   Metal ions in biological system-vanadium and its role in life,
RL   pp.31:325-362, Marcel Dekker, New York (1995).
CC   -!- CATALYTIC ACTIVITY: Halide + H(2)O(2) + H(+) = HOHal + H(2)O.
CC   -!- COFACTOR: VANADIUM.
CC   -!- SUBUNIT: HOMODIMER LINKED BY TWO INTERCHAIN DISULFIDE BONDS.
CC   -!- SIMILARITY: TO OTHER BACTERIAL NON-HEME BROMO- AND CHLORO-
CC       PEROXIDASES.
DR   PDB; 1QI9; 10-JUN-00.
DR   InterPro; IPR000326; PA_PTPase.
KW   Oxidoreductase; Peroxidase; Vanadium; 3D-structure.
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     3      3       INTERCHAIN (WITH C-41 OF OTHER CHAIN).
FT   DISULFID    41     41       INTERCHAIN (WITH C-3 OF OTHER CHAIN).
FT   DISULFID    77     86
FT   DISULFID   441    462
FT   DISULFID   544    555
FT   ACT_SITE   411    411
FT   ACT_SITE   418    418
FT   METAL      486    486       VANADIUM.
FT   CONFLICT   321    321       S -> D (IN REF. 2).
FT   CONFLICT   341    341       K -> N (IN REF. 2; DNA SEQUENCE).
FT   CONFLICT   403    404       AI -> VY (IN REF. 2; DNA SEQUENCE).
FT   CONFLICT   407    408       GS -> T (IN REF. 2).
FT   CONFLICT   409    409       P -> S (IN REF. 2; AA SEQUENCE).
FT   CONFLICT   441    444       CYPD -> AIR (IN REF. 2).
FT   CONFLICT   470    470       N -> K (IN REF. 2).
SQ   SEQUENCE   557 AA;  60343 MW;  E3D8557AB92B16F4 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 557;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKLVFFAE 10
          ||:|: |||
Db    507 HQELMTFAE 515


RESULT 47
YAWG_SCHPO
ID   YAWG_SCHPO     STANDARD;      PRT;   616 AA.
AC   Q10190;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical GTP-binding protein C3F10.16C in chromosome I.
GN   SPAC3F10.16C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE MMR1/HSR1 FAMILY OF GTP-BINDING
CC       PROTEINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; Z69369; CAA93314.1; -.
DR   InterPro; IPR002917; MMR_HSR1.
DR   Pfam; PF01926; MMR_HSR1; 1.
KW   Hypothetical protein; GTP-binding.
FT   NP_BIND     308    315       GTP (POTENTIAL).
FT   NP_BIND     352    356       GTP (POTENTIAL).
SQ   SEQUENCE   616 AA;  69674 MW;  F02A2996AF06FB68 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 616;
  Best Local Similarity   83.3%;  Pred. No. 81;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||:|
Db     480 HHQKIV 485


RESULT 48
GLGB_AGRTU
ID   GLGB_AGRTU     STANDARD;      PRT;   734 AA.
AC   P52979;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
DE   enzyme).
GN   GLGB.
OS   Agrobacterium tumefaciens.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=358;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A348;
RX   MEDLINE=99069330; PubMed=9851999;
RA   Ugalde J.E., Lepek V., Uttaro A.D., Estrella J., Iglesias A.,
RA   Ugalde R.A.;
RT   "Gene organization and transcription analysis of the Agrobacterium
RT   tumefaciens glycogen (glg) operon: two transcripts for the single
RT   phosphoglucomutase gene.";
RL   J. Bacteriol. 180:6557-6564(1998).
CC   -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
CC       glycogen.
CC   -!- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC       KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF033856; AAD03472.1; -.
DR   InterPro; IPR000461; Alpha_amylase.
DR   InterPro; IPR004193; isoamylase_N.
DR   Pfam; PF00128; alpha-amylase; 1.
DR   Pfam; PF02922; isoamylase_N; 1.
KW   Glycogen biosynthesis; Transferase; Glycosyltransferase.
FT   ACT_SITE    417    417       BY SIMILARITY.
FT   ACT_SITE    470    470       BY SIMILARITY.
FT   ACT_SITE    538    538       BY SIMILARITY.
SQ   SEQUENCE   734 AA;  83623 MW;  70A3CD35A77F31E6 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 734;
  Best Local Similarity   71.4%;  Pred. No. 97;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVF 7
           |||:| |
Db     515 HHQELTF 521


RESULT 49
PLD_PIMBR
ID   PLD_PIMBR      STANDARD;      PRT;   808 AA.
AC   O04883;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Phospholipase D precursor (EC 3.1.4.4) (PLD) (Choline phosphatase)
DE   (Phosphatidylcholine-hydrolyzing phospholipase D).
GN   PLD.
OS   Pimpinella brachycarpa.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids II; Apiales; Apiaceae; Pimpinella.
OX   NCBI_TaxID=45043;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cha Y.Y., Lee K.-W., Kim J.C., Han T.J., Lee W.S., Cho S.H.;
RT   "Nucleotide sequence of a cDNA encoding phospholipase D from
RT   Pimpinella brachycarpa.";
RL   (In) Plant Gene Register PGR97-092.
CC   -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN VARIOUS CELLULAR PROCESSES.
CC   -!- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O = choline + a
CC       phosphatidate.
CC   -!- COFACTOR: CALCIUM (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 PLDC DOMAINS.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U96438; AAB70463.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001736; PLD.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00614; PLDc; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00155; PLDc; 2.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Repeat.
FT   PROPEP        1      ?       POTENTIAL.
FT   CHAIN         ?    808       PHOSPHOLIPASE D.
FT   DOMAIN        1    109       C2 DOMAIN.
FT   DOMAIN      326    364       PLDC 1.
FT   DOMAIN      654    681       PLDC 2.
SQ   SEQUENCE   808 AA;  91672 MW;  E83DA015B06F2164 CRC64;

  Query Match             58.2%;  Score 32;  DB 1;  Length 808;
  Best Local Similarity   83.3%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||:|
Db     330 HHQKIV 335


RESULT 50
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PLD_RICCO
ID   PLD_RICCO      STANDARD;      PRT;   808 AA.
AC   Q41142; P93507;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Phospholipase D precursor (EC 3.1.4.4) (PLD) (Choline phosphatase)
DE   (Phosphatidylcholine-hydrolyzing phospholipase D).
OS   Ricinus communis (Castor bean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX   NCBI_TaxID=3988;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=CV. HALE; TISSUE=Endosperm;
RX   MEDLINE=94327597; PubMed=8051126;
RA   Wang X., Xu L., Zheng L.;
RT   "Cloning and expression of phosphatidylcholine-hydrolyzing
RT   phospholipase D from Ricinus communis L.";
RL   J. Biol. Chem. 269:20312-20317(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leaf;
RX   MEDLINE=97134969; PubMed=8980529;
RA   Xu L., Zheng L., Coughlan S.J., Wang X.;
RT   "Structure and analysis of phospholipase D gene from Ricinus communis
RT   L.";
RL   Plant Mol. Biol. 32:767-771(1996).
CC   -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN CELLULAR PATHWAYS INCLUDING
CC       SIGNAL TRANSDUCTION PATHWAYS.
CC   -!- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O = choline + a
CC       phosphatidate.
CC   -!- COFACTOR: CALCIUM (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: MOSTLY EXPRESSED IN VACUOLES, ENDOPLASMIC
CC       RETICULUM, A FEW IN PLASTIDS AND PLASMA MEMBRANE. EXPRESSION IS
CC       HIGHER IN RADICLE THAN IN ENDOSPERM.
CC   -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 PLDC DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L33686; AAB04095.1; -.
DR   EMBL; U72693; AAB37305.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001736; PLD.
DR   Pfam; PF00614; PLDc; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00155; PLDc; 2.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Repeat.
FT   PROPEP        1     30
FT   CHAIN        31    808       PHOSPHOLIPASE D.
FT   DOMAIN        1    109       C2 DOMAIN.
FT   DOMAIN      326    364       PLDC 1.
FT   DOMAIN      654    681       PLDC 2.
FT   CONFLICT    268    268       L -> I (IN REF. 2).
SQ   SEQUENCE   808 AA;  91992 MW;  E75F6CFFB9ADF3CB CRC64;

  Query Match          58.2%;  Score 32;  DB 1;  Length 808;
  Best Local Similarity   83.3%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLV 6
          ||||:|
Db    330 HHQKIV 335
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Search completed: October 29, 2002, 09:24:48
Job time : 15 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:27 ; Search time 25 Seconds
(without alignments)
69.198 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	28	4	Q9UCD1	Q9ucd1 homo sapien
2	55	100.0	30	4	Q9UCA9	Q9uca9 homo sapien
3	55	100.0	33	4	Q9UC33	Q9uc33 homo sapien
4	55	100.0	82	4	P78438	P78438 homo sapien
5	55	100.0	82	4	Q16014	Q16014 homo sapien
6	55	100.0	82	4	Q16019	Q16019 homo sapien
7	55	100.0	82	4	Q16020	Q16020 homo sapien
8	55	100.0	97	4	Q13778	Q13778 homo sapien
9	55	100.0	534	13	O93296	O93296 gallus gall
10	55	100.0	569	13	Q9PVL1	Q9pvl1 gallus gall
11	55	100.0	693	13	Q98SG0	Q98sg0 xenopus lae
12	55	100.0	695	6	Q95KN7	Q95kn7 macaca fasc
13	55	100.0	695	11	Q60496	Q60496 cavia sp. p
14	55	100.0	695	13	Q9DGJ8	Q9dgj8 gallus gall
15	55	100.0	747	13	Q91963	Q91963 xenopus. ap
16	55	100.0	751	13	Q9DGJ7	Q9dgj7 gallus gall
17	55	100.0	770	6	Q9TUI0	Q9tui0 sus scrofa
18	55	100.0	780	13	O73683	O73683 tetraodon f
19	52	94.5	695	13	Q98SF9	Q98sf9 xenopus lae
20	49	89.1	612	13	Q9I9E7	Q9i9e7 brachydanio
21	49	89.1	738	13	Q90W28	Q90w28 brachydanio
22	47	85.5	79	11	O35463	O35463 cricetulus
23	47	85.5	607	11	Q99K32	Q99k32 mus musculu
24	47	85.5	695	11	P97487	P97487 mus musculu
25	46	83.6	699	13	O57394	O57394 narke japon
26	46	83.6	737	13	O93279	O93279 fugu rubrip
27	40	72.7	19	4	Q9UCC8	Q9ucc8 homo sapien
28	39	70.9	1145	5	Q965N2	Q965n2 caenorhabdi
29	38	69.1	272	16	P96882	P96882 mycobacteri
30	38	69.1	326	2	Q9K376	Q9k376 escherichia
31	38	69.1	326	2	Q9K328	Q9k328 escherichia
32	38	69.1	326	2	Q9K2T3	Q9k2t3 escherichia
33	38	69.1	326	2	Q9K2R7	Q9k2r7 escherichia
34	38	69.1	326	2	Q9K2Q3	Q9k2q3 escherichia
35	38	69.1	326	2	Q9KH87	Q9kh87 escherichia
36	38	69.1	326	2	Q9KH85	Q9kh85 escherichia
37	38	69.1	326	2	Q9KH84	Q9kh84 escherichia
38	37	67.3	191	10	Q9SN52	Q9sn52 arabidopsis
39	37	67.3	584	5	Q9U0M8	Q9u0m8 plasmodium
40	37	67.3	1035	2	Q93E19	Q93e19 acinetobact
41	36	65.5	103	6	Q9XST6	Q9xst6 canis famil
42	36	65.5	152	11	Q9CUY7	Q9cuy7 mus musculu
43	36	65.5	190	11	Q9CPW6	Q9cpw6 mus musculu
44	36	65.5	204	11	Q9D8C2	Q9d8c2 mus musculu
45	36	65.5	210	11	Q9CQ88	Q9cq88 mus musculu
46	36	65.5	226	11	Q9CZI6	Q9czi6 mus musculu
47	36	65.5	396	4	Q9UL10	Q9ul10 homo sapien
48	36	65.5	535	3	Q01165	Q01165 magnaporthe
49	36	65.5	859	17	O26556	O26556 methanother
50	36	65.5	1668	17	O27011	O27011 methanother

ALIGNMENTS

RESULT 1
Q9UCD1
ID Q9UCD1 PRELIMINARY; PRT; 28 AA.
AC Q9UCD1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94045685; PubMed=8229004;
RA Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT "Characterization of beta-amyloid peptide from human cerebrospinal
RT fluid.";
RL J. Neurochem. 61:1965-1968(1993).
DR HSSP; P05067; 1AMB.
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22
```

RESULT 2
Q9UCA9
ID Q9UCA9 PRELIMINARY; PRT; 30 AA.

```
AC   Q9UCA9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   BETA-AMYLOID PROTEIN (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94153015; PubMed=8109908;
RA   Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT   "The amino acid sequence of neuritic plaque amyloid from a familial
RT   Alzheimer's disease patient.";
RL   Ann. Neurol. 35:245-246(1994).
DR   HSSP; P05067; 1BA4.
SQ   SEQUENCE   30 AA;  3391 MW;  FF4167ABD081160A CRC64;

  Query Match             100.0%;  Score 55;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.00053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 3
Q9UC33
ID   Q9UC33      PRELIMINARY;      PRT;    33 AA.
AC   Q9UC33;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   BETA-AMYLOID PEPTIDE (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93024877; PubMed=1406936;
RA   Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA   Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT   "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT   biological fluids.";
RL   Nature 359:325-327(1992).
DR   HSSP; P05067; 1BA4.
SQ   SEQUENCE   33 AA;  3674 MW;  B1DEFE2F4167ABD0 CRC64;

  Query Match             100.0%;  Score 55;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.00058;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 4
P78438
ID   P78438      PRELIMINARY;      PRT;    82 AA.
AC   P78438;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN   APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89392030; PubMed=2675837;
RA   Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA   Little S.P.;
RT   "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT   similarity to soybean trypsin inhibitor.";
RL   Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN   [2]
RP   SEQUENCE OF 19-48 FROM N.A.
RX   MEDLINE=87120329; PubMed=2949367;
RA   Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA   Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT   "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT   linkage near the Alzheimer locus.";
RL   Science 235:880-884(1987).
RN   [3]
RP   SEQUENCE OF 32-63 FROM N.A.
RX   MEDLINE=93035397; PubMed=1415269;
RA   Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
RA   Anderson L., O'dahl S., Nemens E., White J.A.;
RT   "Linkage and mutational analysis of familial Alzheimer disease
RT   kindreds for the APP gene region.";
RL   Am. J. Hum. Genet. 51:998-1014(1992).
DR   EMBL; M29270; AAA51768.1; -.
DR   EMBL; M29269; AAA51768.1; JOINED.
DR   EMBL; M15532; AAA51564.1; -.
DR   EMBL; S45136; AAB23646.1; -.
DR   HSSP; P05067; 1BA4.
FT   NON_TER       1      1
SQ   SEQUENCE   82 AA;  8994 MW;  8DA9E42B813A070E CRC64;

  Query Match             100.0%;  Score 55;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.0014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      29 HHQKLVFFAE 38


RESULT 5
Q16014
ID   Q16014      PRELIMINARY;      PRT;    82 AA.
AC   Q16014;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-AMYLOID PEPTIDE (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S60721; AAB26263.2; -.
DR   HSSP; P05067; 1BA4.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8972 MW;  F534AA5B3EA9230A CRC64;

  Query Match             100.0%;  Score 55;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.0014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      30 HHQKLVFFAE 39
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RESULT 6
Q16019
ID   Q16019      PRELIMINARY;      PRT;    82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-AMYLOID PEPTIDE (FRAGMENT).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.
DR   HSSP; P05067; 1BA4.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8938 MW;  F534AA50E579230A CRC64;

  Query Match             100.0%;  Score 55;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.0014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     30 HHQKLVFFAE 39


RESULT 7
Q16020
ID   Q16020      PRELIMINARY;      PRT;    82 AA.
AC   Q16020;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-AMYLOID PEPTIDE (FRAGMENT).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61383; AAB26265.2; -.
DR   HSSP; P05067; 1BA4.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8882 MW;  F534AA5AE5D9230A CRC64;

  Query Match             100.0%;  Score 55;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.0014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     30 HHQKLVFFAE 39


RESULT 8
Q13778
ID   Q13778      PRELIMINARY;      PRT;    97 AA.
AC   Q13778;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87120328; PubMed=3810169;
RA   Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
RT   "Characterization and chromosomal localization of a cDNA encoding
RT   brain amyloid of Alzheimer's disease.";
RL   Science 235:877-880(1987).
DR   EMBL; M15533; AAA35540.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   PRINTS; PR00203; AMYLOIDA4.
FT   NON_TER       1      1
SQ   SEQUENCE   97 AA;  10884 MW;  E528CDB448DE474E CRC64;

  Query Match             100.0%;  Score 55;  DB 4;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     11 HHQKLVFFAE 20


RESULT 9
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID PROTEIN (FRAGMENT).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             100.0%;  Score 55;  DB 13;  Length 534;
  Best Local Similarity   100.0%;  Pred. No. 0.0095;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    448 HHQKLVFFAE 457
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RESULT 10
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID PROTEIN (FRAGMENT).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             100.0%;  Score 55;  DB 13;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db     484 HHQKLVFFAE 493


RESULT 11
Q98SG0
ID   Q98SG0      PRELIMINARY;      PRT;   693 AA.
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-AMYLOID PRECURSOR PROTEIN A.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298150; CAC37193.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   693 AA;  78568 MW;  CAF1DF655C1AB653 CRC64;

  Query Match             100.0%;  Score 55;  DB 13;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db     607 HHQKLVFFAE 616


RESULT 12
Q95KN7
ID   Q95KN7      PRELIMINARY;      PRT;   695 AA.
AC   Q95KN7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID B-PROTEIN PRECURSOR.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CEREBELLUM;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
DR   EMBL; M58727; AAA36829.1; -.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN       597    636       POTENTIAL.
SQ   SEQUENCE   695 AA;  78663 MW;  4F6EA0139F969D56 CRC64;

  Query Match             100.0%;  Score 55;  DB 6;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db     609 HHQKLVFFAE 618


RESULT 13
Q60496
ID   Q60496      PRELIMINARY;      PRT;   695 AA.
AC   Q60496;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS   Cavia sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10143;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
DR   EMBL; X97631; CAA66230.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78701 MW;  5196A0C4017F16AB CRC64;
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  Query Match             100.0%;  Score 55;  DB 11;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    609 HHQKLVFFAE 618


RESULT 14
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             100.0%;  Score 55;  DB 13;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    609 HHQKLVFFAE 618


RESULT 15
Q91963
ID   Q91963      PRELIMINARY;      PRT;   747 AA.
AC   Q91963;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   APP747.
GN   APP747.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93129227; PubMed=1282805;
RA   Okado H., Okamoto H.;
RT   "A Xenopus homologue of the human beta-amyloid precursor protein:
RT   developmental regulation of its gene expression.";
RL   Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR   EMBL; S52417; AAB24853.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor.
SQ   SEQUENCE   747 AA;  84893 MW;  A75E81885681D948 CRC64;

  Query Match             100.0%;  Score 55;  DB 13;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    661 HHQKLVFFAE 670


RESULT 16
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             100.0%;  Score 55;  DB 13;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    665 HHQKLVFFAE 674


RESULT 17
Q9TUI0
ID   Q9TUI0      PRELIMINARY;      PRT;   770 AA.
AC   Q9TUI0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID PRECURSOR PROTEIN.
OS   Sus scrofa (Pig).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid Precursor Protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB032550; BAA84580.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor.
SQ   SEQUENCE   770 AA;  86961 MW;  5F7A1DCB2BCC583E CRC64;

  Query Match           100.0%;  Score 55;  DB 6;  Length 770;
  Best Local Similarity  100.0%;  Pred. No. 0.014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    684 HHQKLVFFAE 693
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RESULT 18
O73683
ID   O73683      PRELIMINARY;      PRT;   780 AA.
AC   O73683;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS:
DE   BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
CC       BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                 HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE945201910 CRC64;

  Query Match           100.0%;  Score 55;  DB 13;  Length 780;
  Best Local Similarity  100.0%;  Pred. No. 0.014;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db    694 HHQKLVFFAE 703
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RESULT 19
Q98SF9
ID   Q98SF9      PRELIMINARY;      PRT;   695 AA.
AC   Q98SF9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-AMYLOID PRECURSOR PROTEIN B.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298151; CAC37194.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   695 AA;  78803 MW;  DC14EB02AFB0204A CRC64;

  Query Match            94.5%;  Score 52;  DB 13;  Length 695;
  Best Local Similarity  90.0%;  Pred. No. 0.049;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          |||||||||:
Db    609 HHQKLVFFAD 618
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RESULT 20
Q9I9E7
ID   Q9I9E7      PRELIMINARY;      PRT;   612 AA.
AC   Q9I9E7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID PROTEIN (FRAGMENT).
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Slavov D.B., Gardiner K.;
RT   "An App cDNA from Zebrafish (Danio rerio).";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF257742; AAF71748.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   612 AA;  69710 MW;  59A9ACBDF9C59EFF CRC64;

  Query Match             89.1%;  Score 49;  DB 13;  Length 612;
  Best Local Similarity   90.0%;  Pred. No. 0.17;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           :|||||||||
Db     526 YHQKLVFFAE 535


RESULT 21
Q90W28
ID   Q90W28      PRELIMINARY;      PRT;   738 AA.
AC   Q90W28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID PRECURSOR PROTEIN.
GN   APP.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Expression analysis of zebrafish app.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389401; AAK64495.1; -.
SQ   SEQUENCE   738 AA;  83577 MW;  AF480F6D308FD298 CRC64;

  Query Match             89.1%;  Score 49;  DB 13;  Length 738;
  Best Local Similarity   90.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           :|||||||||
Db     652 YHQKLVFFAE 661


RESULT 22
O35463
ID   O35463      PRELIMINARY;      PRT;    79 AA.
AC   O35463;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN   BETA APP.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sambamurti K., Pinnix I., Gandhi S.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030413; AAB86608.1; -.
DR   HSSP; P05067; 1BA4.
FT   NON_TER      1      1
FT   NON_TER     79     79
SQ   SEQUENCE   79 AA;  8538 MW;  37F2C6C3BFF3F597 CRC64;

  Query Match             85.5%;  Score 47;  DB 11;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           |||||||||
Db      34 HQKLVFFAE 42


RESULT 23
Q99K32
ID   Q99K32      PRELIMINARY;      PRT;   607 AA.
AC   Q99K32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC   TISSUE.;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005490; AAH05490.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Hypothetical protein; Serine protease inhibitor.
FT   NON_TER      1      1
SQ   SEQUENCE   607 AA;  68391 MW;  BF802214CBA7D172 CRC64;

  Query Match             85.5%;  Score 47;  DB 11;  Length 607;
  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           |||||||||
Db     522 HQKLVFFAE 530
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RESULT 24
P97487
ID   P97487      PRELIMINARY;      PRT;   695 AA.
AC   P97487; P97942;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HIPPOCAMPAL AMYLOID PROTEIN.
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA   Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 581-662 FROM N.A.
RC   STRAIN=129SV;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U84012; AAB41502.1; -.
DR   EMBL; U82624; AAB40919.1; -.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88059; App.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78414 MW;  9A5FBE2ED261236E CRC64;

  Query Match          85.5%;  Score 47;  DB 11;  Length 695;
  Best Local Similarity  100.0%;  Pred. No. 0.48;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           |||||||||
Db     610 HQKLVFFAE 618


RESULT 25
O57394
ID   O57394      PRELIMINARY;      PRT;   699 AA.
AC   O57394;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EL AMYLOID PRECURSOR PROTEIN 699.
GN   EL APP699.
OS   Narke japonica (Electric ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Torpediniformes; Narcinoidei; Narkidae; Narke.
OX   NCBI_TaxID=62965;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=ELECTRIC LOBE;
RX   MEDLINE=98129705; PubMed=9461486;
RA   Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA   Suzuki T.;
RT   "cDNA isolation of Alzheimer's amyloid precursor protein from
RT   cholinergic nerve terminals of the electric organ of the electric
RT   ray.";
RL   Biochem. J. 330:29-33(1998).
DR   EMBL; AB005544; BAA24230.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   699 AA;  78879 MW;  952915C309D50E5C CRC64;

  Query Match          83.6%;  Score 46;  DB 13;  Length 699;
  Best Local Similarity  100.0%;  Pred. No. 0.76;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||||||||
Db     613 HHQKLVFF 620


RESULT 26
O93279
ID   O93279      PRELIMINARY;      PRT;   737 AA.
AC   O93279;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS:
DE   BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN   APP.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC       INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC       G(O) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC       WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC       RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC       NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC       PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
CC       BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL       1    18       POTENTIAL.
FT   CHAIN       19   737       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                              HOMOLOG.
FT   CHAIN      639   681       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN      19   668       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   669   689       POTENTIAL.
FT   DOMAIN     690   737       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     286   344       BPTI/KUNITZ INHIBITOR.
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FT   SITE        726    729       CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE    300    301       REACTIVE BOND.
FT   DISULFID    290    340       BY SIMILARITY.
FT   DISULFID    299    323       BY SIMILARITY.
FT   DISULFID    315    336       BY SIMILARITY.
FT   CARBOHYD    522    522       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   737 AA;  82856 MW;  6FAD01E2E3B2B7E2 CRC64;

  Query Match             83.6%;  Score 46;  DB 13;  Length 737;
  Best Local Similarity   80.0%;  Pred. No. 0.8;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           :|||||||||:
Db     651 YHQKLVFFAD 660


RESULT 27
Q9UCC8
ID   Q9UCC8      PRELIMINARY;      PRT;    19 AA.
AC   Q9UCC8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   BETA-AMYLOID-(1-42) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94068497; PubMed=8248178;
RA   Roher A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA   Gowing E., Ball M.J.;
RT   "beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid
RT   deposits: implications for the pathology of Alzheimer disease.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR   HSSP; P05067; 1AMB.
SQ   SEQUENCE   19 AA;  2315 MW;  05B02B3F6DDECE3E CRC64;

  Query Match             72.7%;  Score 40;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVF 7
             |||||||
Db      13 HHQKLVF 19


RESULT 28
Q965N2
ID   Q965N2      PRELIMINARY;      PRT;  1145 AA.
AC   Q965N2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN BE0003N10.3.
GN   BE0003N10.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC092690; AAK73857.1; -.
SQ   SEQUENCE   1145 AA;  128815 MW;  67EC2437F4F4A377 CRC64;

  Query Match             70.9%;  Score 39;  DB 5;  Length 1145;
  Best Local Similarity   60.0%;  Pred. No. 30;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||:||:|  |
Db     512 HHEKLIFLHE 521


RESULT 29
P96882
ID   P96882      PRELIMINARY;      PRT;   272 AA.
AC   P96882;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 30.1 KDA PROTEIN.
GN   RV3277 OR MTCY71.17.
OS   Mycobacterium tuberculosis.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37RV;
RX   MEDLINE=98295987; PubMed=9634230;
RA   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA   Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA   Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA   Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA   Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA   Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA   Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA   Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT   "Deciphering the biology of Mycobacterium tuberculosis from the
RT   complete genome sequence.";
RL   Nature 393:537-544(1998).
DR   EMBL; Z92771; CAB07080.1; -.
DR   TubercuList; Rv3277; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   272 AA;  30078 MW;  F07597B96A0AB081 CRC64;

  Query Match             69.1%;  Score 38;  DB 16;  Length 272;
  Best Local Similarity   66.7%;  Pred. No. 11;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
             ||: |:|||
Db     137 HHEALLFFA 145


RESULT 30
Q9K376
ID   Q9K376      PRELIMINARY;      PRT;   326 AA.
AC   Q9K376;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CL-3, AND DEC8B;
```

```
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267594; AAF97134.1; -.
DR   EMBL; AF267587; AAF97127.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36326 MW;  326C60E6F59A625C CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     289 HHQKLLSKFFAQ 300


RESULT 31
Q9K328
ID   Q9K328      PRELIMINARY;      PRT;   326 AA.
AC   Q9K328;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=921-B4, CL-37, B170, AND G5506;
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267597; AAF97137.1; -.
DR   EMBL; AF267588; AAF97128.1; -.
DR   EMBL; AF267592; AAF97132.1; -.
DR   EMBL; AF267596; AAF97136.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36333 MW;  51A210E6F59A6248 CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     289 HHQKLLFKFFAQ 300


RESULT 32
Q9K2T3
ID   Q9K2T3      PRELIMINARY;      PRT;   326 AA.
AC   Q9K2T3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DEC12A, AND DEC11A;
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267591; AAF97131.1; -.
DR   EMBL; AF267590; AAF97130.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36347 MW;  A4A740B3F0CF624E CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     289 HHQKLLFKFFAQ 300


RESULT 33
Q9K2R7
ID   Q9K2R7      PRELIMINARY;      PRT;   326 AA.
AC   Q9K2R7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DEC2A, E2348/69, AND DEC1A;
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267581; AAF97121.1; -.
DR   EMBL; AF267579; AAF97119.1; -.
DR   EMBL; AF267580; AAF97120.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36400 MW;  B1B240B3F0CF624E CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     289 HHQKLLFKFFAQ 300
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RESULT 34
Q9K2Q3
ID   Q9K2Q3      PRELIMINARY;      PRT;   326 AA.
AC   Q9K2Q3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DEC5D, 93-111, OK-1, DEC3F, AND 5905;
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267586; AAF97126.1; -.
DR   EMBL; AF267582; AAF97122.1; -.
DR   EMBL; AF267583; AAF97123.1; -.
DR   EMBL; AF267584; AAF97124.1; -.
DR   EMBL; AF267585; AAF97125.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36259 MW;  BC10FECA2EFC1F7A CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     289 HHQKLLSKFFAQ 300


RESULT 35
Q9KH87
ID   Q9KH87      PRELIMINARY;      PRT;   326 AA.
AC   Q9KH87;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DEC9F;
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267589; AAF97129.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36319 MW;  92A210FE5690515A CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     289 HHQKLLFKFFAQ 300


RESULT 36
Q9KH85
ID   Q9KH85      PRELIMINARY;      PRT;   326 AA.
AC   Q9KH85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B2F1;
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267595; AAF97135.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36312 MW;  A905FECA2EFC1F7A CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 HHQKLV--FFAE 10
           |||||:  |||:
Db     289 HHQKLLSKFFAQ 300


RESULT 37
Q9KH84
ID   Q9KH84      PRELIMINARY;      PRT;   326 AA.
AC   Q9KH84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN   PGI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=536;
RX   MEDLINE=20351039; PubMed=10894541;
RA   Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT   "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL   Nature 406:64-67(2000).
DR   EMBL; AF267598; AAF97138.1; -.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
```

```
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW   Isomerase.
FT   NON_TER       1      1
FT   NON_TER     326    326
SQ   SEQUENCE   326 AA;  36340 MW;  C76930B3F0CF625A CRC64;

  Query Match             69.1%;  Score 38;  DB 2;  Length 326;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    2;  Gaps    1;

Qy      1 HHQKLV--FFAE 10
          |||||:  |||:
Db    289 HHQKLLSKFFAQ 300


RESULT 38
Q9SN52
ID   Q9SN52      PRELIMINARY;      PRT;   191 AA.
AC   Q9SN52;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HYPOTHETICAL 21.7 KDA PROTEIN.
GN   F28A21.20 OR AT4G18610.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Mueller M.W., Muendlein A., Felber R., Bancroft I.,
RA   Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Mueller M.W., Muendlein A., Felber R., Mewes H.W., Lemcke K.,
RA   Mayer K.F.X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL035526; CAB37446.1; -.
DR   EMBL; AL161549; CAB78863.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   191 AA;  21744 MW;  DFB6D3495AEB132F CRC64;

  Query Match             67.3%;  Score 37;  DB 10;  Length 191;
  Best Local Similarity   60.0%;  Pred. No. 12;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          |||  ||| :
Db     86 HHQACVFFGQ 95


RESULT 39
Q9U0M8
ID   Q9U0M8      PRELIMINARY;      PRT;   584 AA.
AC   Q9U0M8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 71.0 KDA PROTEIN.
GN   MAL1P3.09.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3D7;
RA   Bowman S., Churcher C., Harris B., Harris D., Lawson D., Quail M.,
RA   Barrell B.;
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL031746; CAB63564.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   584 AA;  70984 MW;  6E06F4C58A08F838 CRC64;

  Query Match             67.3%;  Score 37;  DB 5;  Length 584;
  Best Local Similarity   50.0%;  Pred. No. 38;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          |||| ::| :
Db    528 HHQKTMYFTQ 537


RESULT 40
Q93E19
ID   Q93E19      PRELIMINARY;      PRT;  1035 AA.
AC   Q93E19;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ADEB RND PROTEIN.
GN   ADEB.
OS   Acinetobacter baumannii.
OC   Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC   Acinetobacter.
OX   NCBI_TaxID=470;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BM4454;
RA   Magnet S., Courvalin P., Lambert T.;
RT   "Characterization of a RND type efflux pump involved in aminoglycoside
RT   resistance in Acinetobacter baumannii clinical isolate.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF370885; AAL14440.1; -.
SQ   SEQUENCE   1035 AA;  112614 MW;  928E7935D84BFCF3 CRC64;

  Query Match             67.3%;  Score 37;  DB 2;  Length 1035;
  Best Local Similarity   77.8%;  Pred. No. 68;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFA 9
          ||||  |||
Db    503 HHQKKGFFA 511


RESULT 41
Q9XST6
ID   Q9XST6      PRELIMINARY;      PRT;   103 AA.
AC   Q9XST6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TRANSMEMBRANE PROTEIN (FRAGMENT).
GN   SAS.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=THYROID;
RX   MEDLINE=20422104; PubMed=10964405;
RA   Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
RA   Christophe D.;
RT   "A method for the large-scale cloning of nuclear proteins and nuclear
RT   targeting sequences on a functional basis.";
RL   Anal. Biochem. 284:231-239(2000).
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DR   EMBL; AJ388529; CAB46831.1; -.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
FT   NON_TER     103    103
SQ   SEQUENCE   103 AA;  10723 MW;  5528A76F35FAC581 CRC64;

  Query Match             65.5%;  Score 36;  DB 6;  Length 103;
  Best Local Similarity   75.0%;  Pred. No. 11;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
            ||| |:||
Db      70 HHQVLLFF 77


RESULT 42
Q9CUY7
ID   Q9CUY7      PRELIMINARY;      PRT;   152 AA.
AC   Q9CUY7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   2700085A14RIK PROTEIN (FRAGMENT).
GN   2700085A14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK013523; BAB28897.1; -.
DR   MGD; MGI:1914375; 2700085A14Rik.
DR   InterPro; IPR000301; Transmem_4.
DR   PRINTS; PR00259; TMFOUR.
FT   NON_TER     152    152
SQ   SEQUENCE   152 AA;  16162 MW;  5815EAA2F83F1B6D CRC64;

  Query Match             65.5%;  Score 36;  DB 11;  Length 152;
  Best Local Similarity   75.0%;  Pred. No. 16;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
            ||| |:||
Db      70 HHQVLLFF 77


RESULT 43
Q9CPW6
ID   Q9CPW6      PRELIMINARY;      PRT;   190 AA.
AC   Q9CPW6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   2700085A14RIK PROTEIN.
GN   2700085A14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK012853; BAB28514.1; -.
DR   EMBL; AK012567; BAB28322.1; -.
DR   MGD; MGI:1914375; 2700085A14Rik.
DR   InterPro; IPR000301; Transmem_4.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   190 AA;  20620 MW;  EFBE9D78DACD6927 CRC64;

  Query Match             65.5%;  Score 36;  DB 11;  Length 190;
  Best Local Similarity   75.0%;  Pred. No. 19;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
            ||| |:||
Db      50 HHQVLLFF 57


RESULT 44
Q9D8C2
ID   Q9D8C2      PRELIMINARY;      PRT;   204 AA.
AC   Q9D8C2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1100001I23RIK PROTEIN.
GN   1100001I23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK008175; BAB25510.1; -.
DR   MGD; MGI:1913359; 1100001I23Rik.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   204 AA;  22219 MW;  76B95421EBCAE5F0 CRC64;

  Query Match             65.5%;  Score 36;  DB 11;  Length 204;
  Best Local Similarity   75.0%;  Pred. No. 21;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||| |:||
Db      70 HHQVLLFF 77


RESULT 45
Q9CQ88
ID   Q9CQ88      PRELIMINARY;      PRT;   210 AA.
AC   Q9CQ88;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   2700085A14RIK PROTEIN.
GN   2700085A14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD, AND EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK014183; BAB29196.1; -.
DR   EMBL; AK012457; BAB28252.1; -.
DR   MGD; MGI:1914375; 2700085A14Rik.
DR   InterPro; IPR000301; Transmem_4.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   210 AA;  22694 MW;  B1CAD508BEBCC9FD CRC64;

  Query Match             65.5%;  Score 36;  DB 11;  Length 210;
  Best Local Similarity   75.0%;  Pred. No. 22;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||| |:||
Db      70 HHQVLLFF 77


RESULT 46
Q9CZI6
ID   Q9CZI6      PRELIMINARY;      PRT;   226 AA.
AC   Q9CZI6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1100001I23RIK PROTEIN.
GN   1100001I23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK012571; BAB28326.1; -.
DR   MGD; MGI:1913359; 1100001I23Rik.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   226 AA;  24566 MW;  684BAC91D7C42DEE CRC64;

  Query Match             65.5%;  Score 36;  DB 11;  Length 226;
  Best Local Similarity   75.0%;  Pred. No. 23;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           ||| |:||
Db      70 HHQVLLFF 77


RESULT 47
Q9UL10
ID   Q9UL10      PRELIMINARY;      PRT;   396 AA.
AC   Q9UL10;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 42.4 KDA PROTEIN.
GN   SARDH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=99375323; PubMed=10444331;
RA   Eschenbrenner M., Schuman Jorns M.;
RT   "Cloning and mapping of the cDNA for human sarcosine dehydrogenase, a
RT   flavoenzyme defective in patients with sarcosinemia.";
RL   Genomics 59:300-308(1999).
DR   EMBL; AF095737; AAD53400.2; -.
DR   InterPro; IPR000927; DAO.
DR   InterPro; IPR000205; NAD_binding.
DR   Pfam; PF01266; DAO; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   396 AA;  42362 MW;  150CA3706476BB69 CRC64;

  Query Match             65.5%;  Score 36;  DB 4;  Length 396;
  Best Local Similarity   62.5%;  Pred. No. 41;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
           || :|:||
Db     348 HHTRLIFF 355


RESULT 48
Q01165
ID   Q01165      PRELIMINARY;      PRT;   535 AA.
AC   Q01165;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   TRANSPOSASE.
OS   Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX   NCBI_TaxID=148305;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TRANSPOSON=POT2;
RX   MEDLINE=95115685; PubMed=7816044;
RA   Kachroo P., Leong S.A., Chattoo B.B.;
RT   "Pot2, an inverted repeat transposon from the rice blast fungus
RT   Magnaporthe grisea.";
RL   Mol. Gen. Genet. 245:339-348(1994).
DR   EMBL; Z33638; CAA83918.1; -.
SQ   SEQUENCE   535 AA;  61079 MW;  A755F73FE6878F47 CRC64;

  Query Match             65.5%;  Score 36;  DB 3;  Length 535;
  Best Local Similarity   77.8%;  Pred. No. 55;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFAE 10
           ||:| ||||
Db      80 HQELRFFAE 88


RESULT 49
O26556
ID   O26556      PRELIMINARY;      PRT;   859 AA.
AC   O26556;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   MAGNESIUM CHELATASE SUBUNIT.
GN   MTH456.
OS   Methanothermobacter thermautotrophicus.
OC   Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC   Methanothermobacter.
OX   NCBI_TaxID=145262;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DELTA H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
DR   EMBL; AE000830; AAB84962.1; -.
DR   InterPro; IPR003672; CobN/Mg_chelatase.
DR   Pfam; PF02514; cobN-Mg_chel; 1.
KW   Complete proteome.
SQ   SEQUENCE   859 AA;  97572 MW;  0C7946B7839EF5ED CRC64;

  Query Match             65.5%;  Score 36;  DB 17;  Length 859;
  Best Local Similarity   66.7%;  Pred. No. 89;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
           ||| | |:|
Db     210 HHQYLAFYA 218


RESULT 50
O27011
ID   O27011      PRELIMINARY;      PRT;  1668 AA.
AC   O27011;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   COBALAMIN BIOSYNTHESIS PROTEIN N.
GN   MTH928.
OS   Methanothermobacter thermautotrophicus.
OC   Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC   Methanothermobacter.
OX   NCBI_TaxID=145262;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DELTA H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
DR   EMBL; AE000868; AAB85426.1; -.
DR   InterPro; IPR003672; CobN/Mg_chelatase.
DR   InterPro; IPR001993; Mitoch_carrier.
DR   Pfam; PF02514; cobN-Mg_chel; 1.
DR   PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   1668 AA;  184731 MW;  73D53E89519EAC00 CRC64;

  Query Match             65.5%;  Score 36;  DB 17;  Length 1668;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFA 9
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Db     792 HHQYLAFYA 800


Search completed: October 29, 2002, 09:25:20
Job time : 28 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:37:12 ; Search time 13 Seconds
(without alignments)
18.789 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 70601

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	46	83.6	9	4	US-09-264-709A-4	Sequence 4, Appli
2	42	76.4	8	2	US-08-612-785B-5	Sequence 5, Appli
3	42	76.4	8	4	US-08-703-675C-28	Sequence 28, Appl
4	42	76.4	8	4	US-08-617-267C-5	Sequence 5, Appli
5	38	69.1	7	2	US-08-612-785B-6	Sequence 6, Appli
6	38	69.1	7	4	US-08-703-675C-29	Sequence 29, Appl
7	38	69.1	7	4	US-08-617-267C-6	Sequence 6, Appli
8	34	61.8	7	1	US-08-127-904-14	Sequence 14, Appl
9	34	61.8	7	1	US-08-397-633A-105	Sequence 105, App
10	34	61.8	7	2	US-08-612-785B-7	Sequence 7, Appli
11	34	61.8	7	4	US-08-703-675C-30	Sequence 30, Appl
12	34	61.8	7	4	US-08-617-267C-7	Sequence 7, Appli
13	34	61.8	7	4	US-09-264-709A-13	Sequence 13, Appl
14	34	61.8	7	5	PCT-US94-10475-14	Sequence 14, Appl
15	34	61.8	8	2	US-08-630-645-1	Sequence 1, Appli
16	34	61.8	8	5	PCT-US96-10220-1	Sequence 1, Appli
17	34	61.8	10	3	US-08-970-833-3	Sequence 3, Appli
18	30	54.5	6	2	US-08-612-785B-8	Sequence 8, Appli
19	30	54.5	6	2	US-08-461-216-3	Sequence 3, Appli
20	30	54.5	6	4	US-08-703-675C-31	Sequence 31, Appl
21	30	54.5	6	4	US-09-242-724-24	Sequence 24, Appl
22	30	54.5	6	4	US-08-617-267C-8	Sequence 8, Appli
23	30	54.5	6	4	US-08-723-661B-3	Sequence 3, Appli
24	29	52.7	6	2	US-08-612-785B-9	Sequence 9, Appli
25	29	52.7	6	2	US-08-612-785B-27	Sequence 27, Appl
26	29	52.7	6	4	US-08-703-675C-32	Sequence 32, Appl
27	29	52.7	6	4	US-08-703-675C-40	Sequence 40, Appl
28	29	52.7	6	4	US-08-617-267C-9	Sequence 9, Appli
29	29	52.7	6	4	US-08-617-267C-27	Sequence 27, Appl
30	27	49.1	6	4	US-09-242-724-27	Sequence 27, Appl
31	27	49.1	6	4	US-09-242-724-30	Sequence 30, Appl
32	26	47.3	4	3	US-08-717-551A-1	Sequence 1, Appli
33	26	47.3	6	4	US-09-242-724-33	Sequence 33, Appl
34	25	45.5	5	1	US-08-127-904-15	Sequence 15, Appl
35	25	45.5	5	2	US-08-612-785B-10	Sequence 10, Appl
36	25	45.5	5	3	US-08-970-833-2	Sequence 2, Appli
37	25	45.5	5	4	US-08-703-675C-46	Sequence 46, Appl
38	25	45.5	5	4	US-09-242-724-25	Sequence 25, Appl
39	25	45.5	5	4	US-09-242-724-26	Sequence 26, Appl
40	25	45.5	5	4	US-08-617-267C-10	Sequence 10, Appl
41	25	45.5	5	4	US-09-264-709A-28	Sequence 28, Appl
42	25	45.5	5	5	PCT-US94-10475-15	Sequence 15, Appl
43	25	45.5	6	2	US-08-612-785B-31	Sequence 31, Appl
44	25	45.5	6	3	US-08-664-379B-19	Sequence 19, Appl
45	25	45.5	6	4	US-08-703-675C-44	Sequence 44, Appl
46	25	45.5	6	4	US-09-242-724-31	Sequence 31, Appl
47	25	45.5	6	4	US-08-617-267C-31	Sequence 31, Appl
48	25	45.5	6	4	US-08-617-267C-43	Sequence 43, Appl
49	25	45.5	8	3	US-08-970-833-4	Sequence 4, Appli
50	24	43.6	5	2	US-08-612-785B-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-09-264-709A-4
; Sequence 4, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
;  APPLICANT:  Roberts, Eugene
;  TITLE OF INVENTION:  Method for Design of Substances that Enhance Memory and
;  TITLE OF INVENTION:  Improve the Quality of Life
;  FILE REFERENCE:  2124-310
;  CURRENT APPLICATION NUMBER: US/09/264,709A
;  CURRENT FILING DATE:  1999-03-09
;  PRIOR APPLICATION NUMBER:  08/797,782
;  PRIOR FILING DATE:  1997-02-07
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-264-709A-4

  Query Match             83.6%;  Score 46;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFF 8
            ||||||||
Db       2 HHQKLVFF 9


RESULT 2
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
```

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;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/612,785B
;       FILING DATE:  Herewith
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/404,831
;       FILING DATE:  14-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/475,579
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  PPI-002CP3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-612-785B-5

  Query Match             76.4%;  Score 42;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFA 9
           ||||||||
Db       1 HQKLVFFA 8


RESULT 3
US-08-703-675C-28
; Sequence 28, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;     APPLICANT:  Findeis, Mark A. et al.
;     TITLE OF INVENTION:  Modulators of -Amyloid Peptide      Aggregation Comprising D-
;     NUMBER OF SEQUENCES:  46
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;       STREET:  28 State Street
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  USA
;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/703,675C
;       FILING DATE:  27-AUG-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/404,831
;       FILING DATE:  14-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/475,579
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/616,081
;       FILING DATE:  14-MAR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kara, Catherine J.
;       REGISTRATION NUMBER:  41,106
;       REFERENCE/DOCKET NUMBER:  PPI-016CP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  28:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-703-675C-28

  Query Match             76.4%;  Score 42;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFA 9
           ||||||||
Db       1 HQKLVFFA 8


RESULT 4
US-08-617-267C-5
; Sequence 5, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;     APPLICANT:  Findeis, Mark A. et al.
;     TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;       STREET:  28 State Street
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  USA
;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/617,267C
;       FILING DATE:  14-MAR-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/404,831
;       FILING DATE:  14-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/475,579
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  PPI-002CP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-617-267C-5

  Query Match             76.4%;  Score 42;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFFA 9
           ||||||||
Db       1 HQKLVFFA 8


RESULT 5
US-08-612-785B-6
; Sequence 6, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-785B-6

  Query Match             69.1%;  Score 38;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFF 8
           |||||||
Db       1 HQKLVFF 7


RESULT 6
US-08-703-675C-29
; Sequence 29, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of -Amyloid Peptide    Aggregation Comprising
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/703,675C
;      FILING DATE:  27-AUG-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/616,081
;      FILING DATE:  14-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kara, Catherine J.
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  PPI-016CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-703-675C-29

  Query Match             69.1%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFF 8
           |||||||
Db       1 HQKLVFF 7


RESULT 7
US-08-617-267C-6
; Sequence 6, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-617-267C-6

  Query Match             69.1%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQKLVFF 8
           |||||||
Db       1 HQKLVFF 7


RESULT 8
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
;  GENERAL INFORMATION:
;    APPLICANT:  Eugene Roberts
;    TITLE OF INVENTION:  Method For Antagonizing
;    TITLE OF INVENTION:  Amnestic Effects of Amyloid n
;    TITLE OF INVENTION:  Protein and Improving the
;    TITLE OF INVENTION:  Quality of Life in Individuals
;    TITLE OF INVENTION:  With Alzheimer Disease
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  City of Hope
;      STREET:  1500 East Duarte Road
;      CITY:  Duarte
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  91010-0269
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3M Double Density 5 1/4" diskette
;      COMPUTER:  Wang PC
;      OPERATING SYSTEM:  MS DOS Version 3.20
;      SOFTWARE:  Microsoft
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,904
;      FILING DATE:  29 September 1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:  No. 5470951e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Irons, Edward S.
;      REGISTRATION NUMBER:  16,541
;      REFERENCE/DOCKET NUMBER:  No. 5470951e
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;      TELEX:  No. 5470951e
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7
;      TYPE:  Amino Acid
;      STRANDEDNESS:
;      TOPOLOGY:  Unknown
US-08-127-904-14

  Query Match             61.8%;  Score 34;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFFAE 10
           |||||||
Db       1 KLVFFAE 7


RESULT 9
US-08-397-633A-105
; Sequence 105, Application US/08397633A
; Patent No. 5773577
;  GENERAL INFORMATION:
;    APPLICANT:  Cappello, Joseph
;    TITLE OF INVENTION:  PRODUCTS COMPRISING SUBSTRATESCAPABLE
;    TITLE OF INVENTION:  OF ENZYMATIC CROSS-LINKING
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,633A
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20,015
;      REFERENCE/DOCKET NUMBER:  A-58848-1/BIR PROP-011-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-397-633A-105

  Query Match             61.8%;  Score 34;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLV 6
           ||||||
Db       2 HHQKLV 7
```

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RESULT 10
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-785B-7

  Query Match             61.8%;  Score 34;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 QKLVFFA 9
           |||||||
Db       1 QKLVFFA 7


RESULT 11
US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of -Amyloid Peptide      Aggregation Comprising D-
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/703,675C
;      FILING DATE:  27-AUG-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/616,081
;      FILING DATE:  14-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kara, Catherine J.
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  PPI-016CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-703-675C-30

  Query Match             61.8%;  Score 34;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 QKLVFFA 9
           |||||||
Db       1 QKLVFFA 7


RESULT 12
US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
```

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;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  PPI-002CP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-617-267C-7

  Query Match             61.8%;  Score 34;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 QKLVFFA 9
          |||||||
Db      1 QKLVFFA 7


RESULT 13
US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
;  APPLICANT:  Roberts, Eugene
;  TITLE OF INVENTION:  Method for Design of Substances that Enhance Memory and
;  TITLE OF INVENTION:  Improve the Quality of Life
;  FILE REFERENCE:  2124-310
;  CURRENT APPLICATION NUMBER: US/09/264,709A
;  CURRENT FILING DATE:  1999-03-09
;  PRIOR APPLICATION NUMBER:  08/797,782
;  PRIOR FILING DATE:  1997-02-07
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-264-709A-13

  Query Match             61.8%;  Score 34;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          |||||||
Db      1 KLVFFAE 7


RESULT 14
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
;  GENERAL INFORMATION:
;    APPLICANT:  Eugene Roberts
;    TITLE OF INVENTION:  Method For
;    TITLE OF INVENTION:  Antagonizing Amnestic
;    TITLE OF INVENTION:  Effects of Amyloid n
;    TITLE OF INVENTION:  Protein and Improving
;    TITLE OF INVENTION:  the Quality of Life
;    TITLE OF INVENTION:  in Individuals
;    TITLE OF INVENTION:  With Alzheimer Disease
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  City of Hope
;      STREET:  1500 East Duarte Road
;      CITY:  Duarte
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  91010-0269
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3M Double Density 5 1/4"
;      MEDIUM TYPE:  diskette
;      COMPUTER:  Wang PC
;      OPERATING SYSTEM:  MS DOS Version 3.20
;      SOFTWARE:  Microsoft
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10475
;      FILING DATE:  16 September 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:  U. S. Application
;    PRIOR APPLICATION DATA:  Serial No.
;    PRIOR APPLICATION DATA:  08/127,904; filed
;    PRIOR APPLICATION DATA:  29 September 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Irons, Edward S.
;      REGISTRATION NUMBER:  16,541
;      REFERENCE/DOCKET NUMBER:  None
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 626-3564 or 783-6030
;      TELEFAX:  (202) 783-6031
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7
;      TYPE:  Amino Acid
;      STRANDEDNESS:
;      TOPOLOGY:  Unknown
PCT-US94-10475-14

  Query Match             61.8%;  Score 34;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFAE 10
          |||||||
Db      1 KLVFFAE 7


RESULT 15
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
;  GENERAL INFORMATION:
;    APPLICANT:  SOTO-JARA, Claudio
;    APPLICANT:  BAUMANN, Marc
;    APPLICANT:  FRANGIONE, Blas
;    TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;    TITLE OF INVENTION:  THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;    TITLE OF INVENTION:  WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 400
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,645
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  YUN, Allen C.
;       REGISTRATION NUMBER:  37,971
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-630-645-1

  Query Match             61.8%;  Score 34;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFFAE 10
           |||||||
Db       1 KLVFFAE 7


RESULT 16
PCT-US96-10220-1
; Sequence 1, Application PC/TUS9610220
;  GENERAL INFORMATION:
;     APPLICANT:
;     TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;     TITLE OF INVENTION:  THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;     TITLE OF INVENTION:  WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;     NUMBER OF SEQUENCES:  26
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BROWDY AND NEIMARK
;       STREET:  419 Seventh Street, N.W., Suite 400
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/10220
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,645
;       FILING DATE:  10-APR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1 PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
PCT-US96-10220-1

  Query Match             61.8%;  Score 34;  DB 5;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFFAE 10
           |||||||
Db       1 KLVFFAE 7


RESULT 17
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 6022859
;  GENERAL INFORMATION:
;     APPLICANT:  Kiessling, Laura L.
;     APPLICANT:  Murphy, Regina M.
;     TITLE OF INVENTION:  INHIBITORS OF BETA-AMYLOID TOXICITY
;     NUMBER OF SEQUENCES:  11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Quarles & Brady
;       STREET:  411 East Wisconsin Avenue
;       CITY:  Milwaukee
;       STATE:  Wisconsin
;       COUNTRY:  U.S.A.
;       ZIP:  53202-4497
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/970,833
;       FILING DATE:
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Baker, Jean C.
;       REGISTRATION NUMBER:  35,433
;       REFERENCE/DOCKET NUMBER:  960296.94291
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (414) 277-5709
;       TELEFAX:  (414) 271-3552
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-970-833-3

  Query Match             61.8%;  Score 34;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.89;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFFAE 10
           |||||||
Db       1 KLVFFAE 7


RESULT 18
US-08-612-785B-8
; Sequence 8, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;     APPLICANT:  Findeis, Mark A. et al.
;     TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;     TITLE OF INVENTION:  Aggregation
;     NUMBER OF SEQUENCES:  40
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  LAHIVE & COCKFIELD
;       STREET:  28 State Street, Suite 510
;       CITY:  Boston
;       STATE:  Massachusetts
```

```
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-785B-8

  Query Match             54.5%;  Score 30;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 QKLVFF 8
           ||||||
Db       1 QKLVFF 6


RESULT 19
US-08-461-216-3
; Sequence 3, Application US/08461216
; Patent No. 5958883
;  GENERAL INFORMATION:
;    APPLICANT:  Snow, A.D.
;    TITLE OF INVENTION:  ANIMAL MODELS OF HUMAN AMYLOIDOSES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson and Kindness
;      STREET:  1420 Fifth Avenue, Suite 2800
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette-5.25 inch, 1.2Mb storage
;      COMPUTER:  IBM PC/386 Compatible
;      OPERATING SYSTEM:  MS-DOS 4.01
;      SOFTWARE:  Word for Windows-t
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,216
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/969,734
;      FILING DATE:  October 23, 1992
;      APPLICATION NUMBER:  07/950,417
;      FILING DATE:  September 23, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Broderick, Thomas F.
;      REGISTRATION NUMBER:  31,332
;      REFERENCE/DOCKET NUMBER:  UOFW-1-6707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-206-682-8100; 1-206-224-0709 (direct)
;      TELEFAX:  1-206-224-0779
;      TELEX:  4938023
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;      DESCRIPTION:  {SYMBOL 98 \f "Symbol"}/A4(12-17);
;      DESCRIPTION:  page 60, line 4-5; page 83, line 33 and 27-28
US-08-461-216-3

  Query Match             54.5%;  Score 30;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKL 5
           |||||
Db       2 HHQKL 6


RESULT 20
US-08-703-675C-31
; Sequence 31, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of -Amyloid Peptide      Aggregation Comprising
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/703,675C
;      FILING DATE:  27-AUG-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/616,081
;      FILING DATE:  14-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kara, Catherine J.
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  PPI-016CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
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```
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-703-675C-31

  Query Match             54.5%;  Score 30;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 QKLVFF 8
           ||||||
Db       1 QKLVFF 6


RESULT 21
US-09-242-724-24
; Sequence 24, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: :
US-09-242-724-24

  Query Match             54.5%;  Score 30;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 QKLVFF 8
           ||||||
Db       1 QKLVFF 6


RESULT 22
US-08-617-267C-8
; Sequence 8, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-617-267C-8

  Query Match             54.5%;  Score 30;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 QKLVFF 8
           ||||||
Db       1 QKLVFF 6


RESULT 23
US-08-723-661B-3
; Sequence 3, Application US/08723661B
; Patent No. 6340783
;   GENERAL INFORMATION:
;        APPLICANT: Alan D Snow
;        TITLE OF INVENTION: Animal Models of Human Amyloidoses
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Patrick M. Dwyer
;             STREET: 1818 Westlake Avenue N, Suite 114
;             CITY: Seattle
;             STATE: WA (Washington)
;             COUNTRY: United States of America
;             ZIP: 98109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
;             COMPUTER: IBM PC
;             OPERATING SYSTEM: PC-DOS (Windows 98)
;             SOFTWARE: WordPerfect 5.2
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/723,661B
;             FILING DATE: 31-Oct-1996
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/461,216
;             FILING DATE: 05-Jun-1995
;             APPLICATION NUMBER: 07/969,734
;             FILING DATE: 23-Oct-1992
;             APPLICATION NUMBER: 07/950,417
;             FILING DATE: 23-Sep-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dwyer, Patrick M.
;             REGISTRATION NUMBER: 32,411
;             REFERENCE/DOCKET NUMBER: PROTEO.P00C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 343-7074
;             TELEFAX: (206) 343-7085
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6 AMINO ACIDS
;             TYPE: AMINO ACID
;             STRANDEDNESS: SINGLE
;             TOPOLOGY: LINEAR
;        MOLECULE TYPE: PEPTIDE
;             DESCRIPTION: /A4 (12-17); page 60, lines 4-5; page 83,
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;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-723-661B-3

  Query Match           54.5%;  Score 30;  DB 4;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKL 5
          |||||
Db      2 HHQKL 6


RESULT 24
US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-785B-9

  Query Match           52.7%;  Score 29;  DB 2;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFA 9
          ||||||
Db      1 KLVFFA 6


RESULT 25
US-08-612-785B-27
; Sequence 27, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-785B-27

  Query Match           52.7%;  Score 29;  DB 2;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVFFAE 10
          ||||||
Db      1 LVFFAE 6


RESULT 26
US-08-703-675C-32
; Sequence 32, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of -Amyloid Peptide      Aggregation Comprising
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/703,675C
;       FILING DATE:  27-AUG-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/404,831
;       FILING DATE:  14-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/475,579
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/616,081
;       FILING DATE:  14-MAR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kara, Catherine J.
;       REGISTRATION NUMBER:  41,106
;       REFERENCE/DOCKET NUMBER:  PPI-016CP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-703-675C-32

  Query Match             52.7%;  Score 29;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFFA 9
           ||||||
Db       1 KLVFFA 6


RESULT 27
US-08-703-675C-40
; Sequence 40, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of -Amyloid Peptide      Aggregation Comprising D-
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/703,675C
;      FILING DATE:  27-AUG-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/616,081
;      FILING DATE:  14-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kara, Catherine J.
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  PPI-016CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-703-675C-40

  Query Match             52.7%;  Score 29;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 LVFFAE 10
             ||||||
Db       1 LVFFAE 6


RESULT 28
US-08-617-267C-9
; Sequence 9, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
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```
;    MOLECULE TYPE:  peptide
US-08-617-267C-9

  Query Match             52.7%;  Score 29;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFFA 9
          ||||||
Db      1 KLVFFA 6


RESULT 29
US-08-617-267C-27
; Sequence 27, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-617-267C-27

  Query Match             52.7%;  Score 29;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVFFAE 10
          ||||||
Db      1 LVFFAE 6


RESULT 30
US-09-242-724-27
; Sequence 27, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: polypeptide
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: ACETYLATION
;   NAME/KEY: MOD_RES
;   LOCATION: (2)
;   OTHER INFORMATION: K(2Cl-Cbz) = 2-chlorobenzyloxycarbonyl-protected
;   OTHER INFORMATION: lysine
US-09-242-724-27

  Query Match             49.1%;  Score 27;  DB 4;  Length 6;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 QKLVFF 8
          :|||||
Db      1 EKLVFF 6


RESULT 31
US-09-242-724-30
; Sequence 30, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: polypeptide
US-09-242-724-30

  Query Match             49.1%;  Score 27;  DB 4;  Length 6;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 QKLVFF 8
          :|||||
Db      1 EKLVFF 6


RESULT 32
US-08-717-551A-1
; Sequence 1, Application US/08717551A
; Patent No. 6071493
;  GENERAL INFORMATION:
;    APPLICANT:  Dana Giulian
;    TITLE OF INVENTION:  Identification of Agents that Protect
;    TITLE OF INVENTION:  Against Inflammatory Injury to Neurons
;    NUMBER OF SEQUENCES:  2
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz
;      ADDRESSEE:  & No. 6071493ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WORDPERFECT for WINDOWS 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/717,551A
;      FILING DATE:  Sept-20-96
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lori Y. Beardell
;      REGISTRATION NUMBER:  34,293
;      REFERENCE/DOCKET NUMBER:  BYLR-0031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-717-551A-1

  Query Match             47.3%;  Score 26;  DB 3;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQK 4
           ||||
Db       1 HHQK 4


RESULT 33
US-09-242-724-33
; Sequence 33, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: polypeptide
US-09-242-724-33

  Query Match             47.3%;  Score 26;  DB 4;  Length 6;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 QKLVFF 8
           :|||||
Db       1 KKLVFF 6


RESULT 34
US-08-127-904-15
; Sequence 15, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
;    APPLICANT:  Eugene Roberts
;    TITLE OF INVENTION:  Method For Antagonizing
;    TITLE OF INVENTION:  Amnestic Effects of Amyloid n
;    TITLE OF INVENTION:  Protein and Improving the
;    TITLE OF INVENTION:  Quality of Life in Individuals
;    TITLE OF INVENTION:  With Alzheimer Disease
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  City of Hope
;      STREET:  1500 East Duarte Road
;      CITY:  Duarte
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  91010-0269
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3M Double Density 5 1/4" diskette
;      COMPUTER:  Wang PC
;      OPERATING SYSTEM:  MS DOS Version 3.20
;      SOFTWARE:  Microsoft
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,904
;      FILING DATE:  29 September 1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:  No. 5470951e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Irons, Edward S.
;      REGISTRATION NUMBER:  16,541
;      REFERENCE/DOCKET NUMBER:  No. 5470951e
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;      TELEX:  No. 5470951e
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5
;      TYPE:  Amino Acid
;      STRANDEDNESS:
;      TOPOLOGY:  Unknown
US-08-127-904-15

  Query Match             45.5%;  Score 25;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFF 8
           |||||
Db       1 KLVFF 5


RESULT 35
US-08-612-785B-10
; Sequence 10, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/612,785B
;       FILING DATE:  Herewith
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/404,831
;       FILING DATE:  14-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/475,579
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  PPI-002CP3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-612-785B-10

  Query Match             45.5%;  Score 25;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFF 8
           |||||
Db       1 KLVFF 5


RESULT 36
US-08-970-833-2
; Sequence 2, Application US/08970833
; Patent No. 6022859
;  GENERAL INFORMATION:
;    APPLICANT:  Kiessling, Laura L.
;    APPLICANT:  Murphy, Regina M.
;    TITLE OF INVENTION:  INHIBITORS OF BETA-AMYLOID TOXICITY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  411 East Wisconsin Avenue
;      CITY:  Milwaukee
;      STATE:  Wisconsin
;      COUNTRY:  U.S.A.
;      ZIP:  53202-4497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/970,833
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baker, Jean C.
;      REGISTRATION NUMBER:  35,433
;      REFERENCE/DOCKET NUMBER:  960296.94291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (414) 277-5709
;      TELEFAX:  (414) 271-3552
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-970-833-2

  Query Match             45.5%;  Score 25;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFF 8
           |||||
Db       1 KLVFF 5


RESULT 37
US-08-703-675C-46
; Sequence 46, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of -Amyloid Peptide      Aggregation Comprising
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/703,675C
;      FILING DATE:  27-AUG-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/616,081
;      FILING DATE:  14-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kara, Catherine J.
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  PPI-016CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-703-675C-46

  Query Match             45.5%;  Score 25;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      4 KLVFF 8
          |||||
Db      1 KLVFF 5


RESULT 38
US-09-242-724-25
; Sequence 25, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: :
US-09-242-724-25

  Query Match             45.5%;  Score 25;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          |||||
Db      1 KLVFF 5


RESULT 39
US-09-242-724-26
; Sequence 26, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 26
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: ACETYLATION; K(2Cl-Cbz) =
;   OTHER INFORMATION: 2-chlorobenzyloxycarbonyl-protected lysine
US-09-242-724-26

  Query Match             45.5%;  Score 25;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          |||||
Db      1 KLVFF 5


RESULT 40
US-08-617-267C-10
; Sequence 10, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-617-267C-10

  Query Match             45.5%;  Score 25;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          |||||
Db      1 KLVFF 5


RESULT 41
US-09-264-709A-28
; Sequence 28, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
;  APPLICANT:  Roberts, Eugene
;  TITLE OF INVENTION:  Method for Design of Substances that Enhance Memory and
;  TITLE OF INVENTION:  Improve the Quality of Life
;  FILE REFERENCE:  2124-310
;  CURRENT APPLICATION NUMBER: US/09/264,709A
;  CURRENT FILING DATE:  1999-03-09
;  PRIOR APPLICATION NUMBER:  08/797,782
;  PRIOR FILING DATE:  1997-02-07
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: memory-modulating peptide
```

```
US-09-264-709A-28

  Query Match             45.5%;  Score 25;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 VFFAE 10
          |||||
Db      1 VFFAE 5


RESULT 42
PCT-US94-10475-15
; Sequence 15, Application PC/TUS9410475
;  GENERAL INFORMATION:
;    APPLICANT:  Eugene Roberts
;    TITLE OF INVENTION:  Method For
;    TITLE OF INVENTION:  Antagonizing Amnestic
;    TITLE OF INVENTION:  Effects of Amyloid n
;    TITLE OF INVENTION:  Protein and Improving
;    TITLE OF INVENTION:  the Quality of Life
;    TITLE OF INVENTION:  in Individuals
;    TITLE OF INVENTION:  With Alzheimer Disease
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  City of Hope
;      STREET:  1500 East Duarte Road
;      CITY:  Duarte
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  91010-0269
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3M Double Density 5 1/4"
;      MEDIUM TYPE:  diskette
;      COMPUTER:  Wang PC
;      OPERATING SYSTEM:  MS DOS Version 3.20
;      SOFTWARE:  Microsoft
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10475
;      FILING DATE:  16 September 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:  U. S. Application
;    PRIOR APPLICATION DATA:  Serial No.
;    PRIOR APPLICATION DATA:  08/127,904; filed
;    PRIOR APPLICATION DATA:  29 September 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Irons, Edward S.
;      REGISTRATION NUMBER:  16,541
;      REFERENCE/DOCKET NUMBER:  None
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 626-3564 or 783-6030
;      TELEFAX:  (202) 783-6031
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5
;      TYPE:  Amino Acid
;      STRANDEDNESS:
;      TOPOLOGY:  Unknown
PCT-US94-10475-15

  Query Match             45.5%;  Score 25;  DB 5;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          |||||
Db      1 KLVFF 5


RESULT 43
US-08-612-785B-31
; Sequence 31, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified site
;      LOCATION:  6
;      OTHER INFORMATION:  /note= Xaa is beta-alanyl
US-08-612-785B-31

  Query Match             45.5%;  Score 25;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          |||||
Db      1 KLVFF 5


RESULT 44
US-08-664-379B-19
; Sequence 19, Application US/08664379B
; Patent No. 6034211
;  GENERAL INFORMATION:
;    APPLICANT:  Kelly, Jeffery W.
;    TITLE OF INVENTION:  BETA-SHEET NUCLEATING PEPTIDOMIMETICS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
```

```
;       ZIP:  02110-2804
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/664,379B
;       FILING DATE:  14-JUN-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/018,925
;       FILING DATE:  03-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Freeman, John W.
;       REGISTRATION NUMBER:  29,066
;       REFERENCE/DOCKET NUMBER:  08435/003001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-542-5070
;       TELEFAX:  617-542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       LOCATION:  1...1
;       OTHER INFORMATION:  wherein Xaa at position 1 is Ornithine
US-08-664-379B-19

  Query Match             45.5%;  Score 25;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFF 8
           |||||
Db       2 KLVFF 6


RESULT 45
US-08-703-675C-44
; Sequence 44, Application US/08703675C
; Patent No. 6303567
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of -Amyloid Peptide      Aggregation Comprising D-
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/703,675C
;      FILING DATE:  27-AUG-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/616,081
;      FILING DATE:  14-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kara, Catherine J.
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  PPI-016CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified site
;      LOCATION:  6
;      OTHER INFORMATION:  /note= Xaa is beta-alanyl
US-08-703-675C-44

  Query Match             45.5%;  Score 25;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFF 8
           |||||
Db       1 KLVFF 5


RESULT 46
US-09-242-724-31
; Sequence 31, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
;  APPLICANT:  Solomon, Michael E.
;  APPLICANT:  Rich, Daniel H.
;  TITLE OF INVENTION:  Cyclosporin A Conjugates and Uses Therefor
;  FILE REFERENCE:  Cyclosporin Analogs
;  CURRENT APPLICATION NUMBER: US/09/242,724
;  CURRENT FILING DATE:  1999-02-22
;  NUMBER OF SEQ ID NOS:  33
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: polypeptide
US-09-242-724-31

  Query Match             45.5%;  Score 25;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVFF 8
           |||||
Db       1 KLVFF 5


RESULT 47
US-08-617-267C-31
; Sequence 31, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
```

```
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  USA
;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/617,267C
;       FILING DATE:  14-MAR-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/404,831
;       FILING DATE:  14-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/475,579
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  PPI-002CP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Modified site
;       LOCATION:  6
;       OTHER INFORMATION:  /note= Xaa is beta-alanyl
US-08-617-267C-31

  Query Match             45.5%;  Score 25;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          |||||
Db      1 KLVFF 5


RESULT 48
US-08-617-267C-43
; Sequence 43, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-617-267C-43

  Query Match             45.5%;  Score 25;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          |||||
Db      2 KLVFF 6


RESULT 49
US-08-970-833-4
; Sequence 4, Application US/08970833
; Patent No. 6022859
;  GENERAL INFORMATION:
;    APPLICANT:  Kiessling, Laura L.
;    APPLICANT:  Murphy, Regina M.
;    TITLE OF INVENTION:  INHIBITORS OF BETA-AMYLOID TOXICITY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  411 East Wisconsin Avenue
;      CITY:  Milwaukee
;      STATE:  Wisconsin
;      COUNTRY:  U.S.A.
;      ZIP:  53202-4497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/970,833
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baker, Jean C.
;      REGISTRATION NUMBER:  35,433
;      REFERENCE/DOCKET NUMBER:  960296.94291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (414) 277-5709
;      TELEFAX:  (414) 271-3552
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-970-833-4
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  Query Match           45.5%;  Score 25;  DB 3;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 VFFAE 10
           |||||
Db       1 VFFAE 5


RESULT 50
US-08-612-785B-11
; Sequence 11, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-785B-11

  Query Match           43.6%;  Score 24;  DB 2;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 LVFFA 9
           |||||
Db       1 LVFFA 5


Search completed: October 29, 2002, 09:39:08
Job time : 14 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:35:42 ; Search time 14 Seconds
(without alignments)
68.635 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1099

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	36.4	5	2	C41225	copper resistance
2	20	36.4	9	2	PT0080	60K Ca binding pro
3	18	32.7	10	2	S65387	cytochrome-c oxida
4	16	29.1	6	2	A46474	Fc epsilon RIIb -
5	16	29.1	9	2	S13889	phosphoenolpyruvat
6	16	29.1	10	2	S74176	gluconokinase (EC
7	15	27.3	8	2	S21273	cellulase (EC 3.2.
8	15	27.3	9	2	A61102	parathyroid hormon
9	15	27.3	9	2	T31612	hypothetical prote
10	15	27.3	9	2	S10920	venom protein HR-3
11	15	27.3	9	2	B39504	octamer-binding pr
12	15	27.3	10	2	PT0310	Ig heavy chain CRD
13	15	27.3	10	2	PH0807	T-cell receptor al
14	14	25.5	7	2	A30812	sex pheromone cCF1
15	14	25.5	9	2	B20569	serum amyloid P-co
16	14	25.5	10	2	PH0113	alpha-amylase (EC
17	14	25.5	10	2	S43631	cytochrome-c oxida
18	13	23.6	4	2	T46627	hypothetical prote
19	13	23.6	6	2	S71349	beta-crystallin B2
20	13	23.6	8	2	PT0368	Ig gamma chain C r
21	13	23.6	9	2	S55696	phosphoenolpyruvat
22	13	23.6	10	2	S65388	cytochrome-c oxida
23	13	23.6	10	2	S30348	clotting protein -
24	13	23.6	10	2	S43625	cytochrome-c oxida
25	13	23.6	10	2	PT0284	Ig heavy chain CRD
26	13	23.6	10	2	B45482	platelet activatin
27	13	23.6	10	2	T13838	cytochrome-c oxida
28	13	23.6	10	2	T13976	cytochrome-c oxida
29	13	23.6	10	2	T17057	cytochrome-c oxida
30	13	23.6	10	2	T12303	cytochrome-c oxida
31	13	23.6	10	2	T14019	cytochrome-c oxida
32	13	23.6	10	2	T17060	cytochrome-c oxida
33	13	23.6	10	2	T14043	cytochrome-c oxida
34	13	23.6	10	2	T14054	cytochrome-c oxida
35	13	23.6	10	2	T17066	cytochrome-c oxida
36	13	23.6	10	2	T17069	cytochrome-c oxida
37	13	23.6	10	2	T12308	cytochrome-c oxida
38	13	23.6	10	2	T17072	cytochrome-c oxida
39	13	23.6	10	2	T12312	cytochrome-c oxida
40	13	23.6	10	2	T12316	cytochrome-c oxida
41	13	23.6	10	2	T12321	cytochrome-c oxida
42	13	23.6	10	2	T14219	cytochrome-c oxida
43	12	21.8	4	2	JQ1273	neuropeptide Antho
44	12	21.8	4	2	A32480	achatin-I - giant
45	12	21.8	6	2	A60986	N-formyl oligopept
46	12	21.8	6	2	I59142	platelet-derived g
47	12	21.8	6	2	A43129	neuropeptide GNFFR
48	12	21.8	7	2	PT0246	Ig heavy chain CRD
49	12	21.8	7	2	I46868	alpha-myosin heavy
50	12	21.8	8	2	T13818	cytochrome oxidase

ALIGNMENTS

RESULT 1
C41225
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: C41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer
A;Reference number: A41225; MUID:92020961
A;Accession: C41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHA>

Query Match 36.4%; Score 20; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 HQKLV 6
           | |||
Db       1 HPKLV 5
```

RESULT 2
PT0080
60K Ca binding protein - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PT0080
R;Treveso, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 444-450, 1991
A;Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calr
A;Reference number: PT0080; MUID:91207333
A;Accession: PT0080
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <TRE>

Query Match 36.4%; Score 20; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       5 LVFF 8
           ||||
Db       3 LVFF 6
```

RESULT 3
S65387
cytochrome-c oxidase (EC 1.9.3.1) chain VII b, cardiac - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
C;Accession: S65387; S65386
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A;Reference number: S65372; MUID:95324529
A;Accession: S65387
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SCH>
A;Accession: S65386
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SC2>
C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 32.7%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQK 4
|||
Db 2 HQK 4

RESULT 4
A46474
Fc epsilon RIIb - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Accession: A46474
R;Richards, M.L.; Katz, D.H.; Liu, F.T.
J. Immunol. 147, 1067-1074, 1991
A;Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Demon
A;Reference number: A46474; MUID:91318149
A;Accession: A46474
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-6 <RIC>
A;Experimental source: BALB C, splenic B cells
A;Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 29.1%; Score 16; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HH 2
||
Db 4 HH 5

RESULT 5
S13889
phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize
C;Species: Zea mays (maize)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C;Accession: S13889
R;Jiao, J.; Chollet, R.
Arch. Biochem. Biophys. 283, 300-305, 1990
A;Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylas
A;Reference number: S13889; MUID:91112741
A;Accession: S13889
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <JIA>
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HH 2
||
Db 1 HH 2

RESULT 6
S74176
gluconokinase (EC 2.7.1.12), thermoresistant - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C;Accession: S74176
R;Izu, H.; Adachi, O.; Yamada, M.
FEBS Lett. 394, 14-16, 1996
A;Title: Purification and characterization of the Escherichia coli thermoresistant gl
A;Reference number: S74176; MUID:97074194
A;Accession: S74176
A;Molecule type: protein
A;Residues: 1-10 <IZU>
A;Experimental source: strain K-12
C;Genetics:
A;Gene: gntK
C;Keywords: dimer; phosphotransferase

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HH 2
||
Db 7 HH 8

RESULT 7
S21273
cellulase (EC 3.2.1.4) - Clostridium thermocellum (fragment)
N;Alternate names: endo-1,4-beta-glucanase
C;Species: Clostridium thermocellum
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 22-Nov-1996
C;Accession: S21273
R;Romaniec, M.P.M.; Fauth, U.; Kobayashi, T.; Huskisson, N.S.; Barker, P.J.; Demain,
Biochem. J. 283, 69-73, 1992
A;Title: Purification and characterization of a new endoglucanase from Clostridium th
A;Reference number: S21273; MUID:92231850
A;Accession: S21273
A;Molecule type: protein
A;Residues: 1-8 <ROM>
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as
A;Pathway: cellulose degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.3%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FAE 10
|||
Db 4 FAE 6

RESULT 8
A61102
parathyroid hormone-like protein, humoral hypercalcemia of malignancy - dog (fragment
C;Species: Canis lupus familiaris (dog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: A61102
R;Weir, E.C.; Burtis, W.J.; Morris, C.A.; Brady, T.G.; Insogna, K.L.
Endocrinology 123, 2744-2751, 1988
A;Title: Isolation of 16,000-Dalton parathyroid hormone-like proteins from two animal
A;Reference number: A61102; MUID:89064600

A;Accession: A61102
A;Molecule type: protein
A;Residues: 1-9 <WEI>
A;Experimental source: apocrine cell adenocarcinoma
C;Superfamily: parathyroid hormone-related protein; parathyroid hormone homology
C;Keywords: hormone; humoral hypercalcemia

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HQKL 5
|| |
Db 6 HQLL 9

RESULT 9
T31612
hypothetical protein Y50E8A.h - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31612
R;Steward, C.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21047
A;Accession: T31612
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-9 <WIL>
A;Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55051.1; CESP:Y50E8A.h
A;Experimental source: clone Y50E8A
C;Genetics:
A;Gene: CESP:Y50E8A.h

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HHQK 4
| :|
Db 5 HREK 8

RESULT 10
S10920
venom protein HR-3 - oriental hornet (fragment)
C;Species: Vespa orientalis (oriental hornet)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 08-Dec-1995
C;Accession: S10920
R;Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St
A;Reference number: S06445
A;Accession: S10920
A;Molecule type: protein
A;Residues: 1-9 <TUI>
C;Keywords: venom

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HQKLV 6
|: ||
Db 4 HEFLV 8

RESULT 11
B39504
octamer-binding protein, Ku-like, 83K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: B39504
R;May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A;Title: Purification and characterization of Ku-2, an octamer-binding protein relate
A;Reference number: A39504; MUID:91131605
A;Accession: B39504
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <MAY>

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LVFFAE 10
:|| |
Db 1 MVFMNE 6

RESULT 12
PT0310
Ig heavy chain CRD3 region (clone 6-97) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0310
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0310
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LVFF 8
||:|
Db 3 LVWF 6

RESULT 13
PH0807
T-cell receptor alpha chain (J4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0807
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility comple
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846
A;Accession: PH0807
A;Molecule type: mRNA
A;Residues: 1-10 <CAS>
A;Cross-references: EMBL:X60916
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VFF 8
:||
Db 7 IFF 9

RESULT 14
A30812
sex pheromone cCF10 - Enterococcus faecalis

C;Species: Enterococcus faecalis
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C;Accession: A30812
R;Mori, M.; Sakagami, Y.; Ishii, Y.; Isogai, A.; Kitada, C.; Fujino, M.; Adsit, J.C.; Du
J. Biol. Chem. 263, 14574-14578, 1988
A;Title: Structure of cCF10, a peptide sex pheromone which induces conjugative transfer
A;Reference number: A30812; MUID:89008313
A;Accession: A30812
A;Molecule type: protein
A;Residues: 1-7 <MOR>

Query Match 25.5%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LVF 7
|||
Db 4 LVF 6

RESULT 15
B20569
serum amyloid P-component - smooth dogfish (fragment)
C;Species: Mustelus canis (smooth dogfish)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993
C;Accession: B20569; A05074
R;Robey, F.A.; Tanaka, T.; Liu, T.Y.
J. Biol. Chem. 258, 3889-3894, 1983
A;Title: Isolation and characterization of two major serum proteins from the dogfish, Mu
A;Reference number: A92419; MUID:83160932
A;Accession: B20569
A;Molecule type: protein
A;Residues: 1-9 <ROB>
C;Keywords: amyloid

Query Match 25.5%; Score 14; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QKLVF 7
: |:| .
Db 5 KSLIF 9

RESULT 16
PH0113
alpha-amylase (EC 3.2.1.1) III - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 07-May-1999
C;Accession: PH0113
R;Chiba, Y.; Nieda, Y.; Nakajima, T.; Ichishima, E.
Agric. Biol. Chem. 55, 901-902, 1991
A;Title: Unique enzymatic properties of alpha-amylase-III from suspension-cultured rice
A;Reference number: PH0113; MUID:91234351
A;Accession: PH0113
A;Molecule type: protein
A;Residues: 1-10 <CHI>
A;Experimental source: cv. Sasanishiki
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 25.5%; Score 14; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKLV 6
|:||
Db 6 QELV 9

RESULT 17
S43631
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, cardiac - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C;Accession: S43631
R;Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytoc
A;Reference number: S43624; MUID:94237150
A;Accession: S43631
A;Molecule type: protein
A;Residues: 1-10 <FRE>
A;Note: the source is designated as Salmo gairdneri
C;Genetics:
A;Genome: nuclear
C;Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidor

Query Match 25.5%; Score 14; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKL 5
|||
Db 8 QKL 10

RESULT 18
T46627
hypothetical protein c4 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is
A;Reference number: Z23105
A;Accession: T46627
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4 <CHA>
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 23.6%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KLV 6
|||
Db 2 KLV 4

RESULT 19
S71349
beta-crystallin B2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 07-May-1999
C;Accession: S71349
R;Dirks, R.P.H.; Kraft, H.J.; van Genesen, S.T.; Klok, E.J.; Pfundt, R.; Schoenmakers
Eur. J. Biochem. 239, 23-32, 1996
A;Title: The cooperation between two silencers creates an enhancer element that contr
A;Reference number: S71349; MUID:96305362
A;Accession: S71349
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <DIR>
A;Cross-references: EMBL:X83671
A;Experimental source: strain Wistar; lens epithelial cells
C;Genetics:
A;Gene: CRYBB2

Query Match 23.6%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

```
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQ 3
          ||
Db      5 HQ 6


RESULT 20
PT0368
Ig gamma chain C region (gamma-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
C;Accession: PT0368
R;Milili, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.
Mol. Immunol. 28, 753-761, 1991
A;Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.
A;Reference number: PT0368; MUID:91312348
A;Accession: PT0368
A;Molecule type: mRNA
A;Residues: 1-8 <MIL>
A;Experimental source: fetal liver
C;Keywords: immunoglobulin

  Query Match             23.6%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQ 3
          ||
Db      2 HQ 3


RESULT 21
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S55696
R;Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A;Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try
A;Reference number: S55696; MUID:95284106
A;Accession: S55696
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <HUN>

  Query Match             23.6%;  Score 13;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKL 5
          |: |
Db      5 HKNL 8


RESULT 22
S65388
cytochrome-c oxidase (EC 1.9.3.1) chain VII c, hepatic - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S65388; S65389
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A;Reference number: S65372; MUID:95324529
A;Accession: S65388
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SCH>
A;Accession: S65389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SC2>
C;Superfamily: cytochrome-c oxidase chain VIIc
C;Keywords: oxidoreductase

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 1.7e+04;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQK 4
          |:::
Db      2 HYEE 5


RESULT 23
S30348
clotting protein - signal crayfish
C;Species: Pacifastacus leniusculus (signal crayfish)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S30348
R;Kopacek, P.; Hall, M.; Soederhaell, K.
Eur. J. Biochem. 213, 591-597, 1993
A;Title: Characterization of a clotting protein, isolated from plasma of the freshwat
A;Reference number: S30348; MUID:93238739
A;Accession: S30348
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <KOP>

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 HQKLVF 7
          |  | :
Db      2 HSNLEY 7


RESULT 24
S43625
cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S43625
R;Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytoc
A;Reference number: S43624; MUID:94237150
A;Accession: S43625
A;Molecule type: protein
A;Residues: 1-10 <FRE>
A;Note: the source is designated as Salmo gairdneri
C;Genetics:
A;Genome: nuclear
C;Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKL 5
          | |:
Db      2 HAKV 5


RESULT 25
PT0284
Ig heavy chain CRD3 region (clone 4-97) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0284
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
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A;Reference number: PT0222; MUID:91108337
A;Accession: PT0284
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 QKLVFF 8
          |:|  |
Db      3 QQLANF 8


RESULT 26
B45482
platelet activating factor acetylhydrolase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 05-May-1995
C;Accession: B45482
R;Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.
J. Biol. Chem. 268, 3857-3865, 1993
A;Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Purific
A;Reference number: A45482; MUID:93179380
A;Accession: B45482
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <STA>

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+04;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          || |
Db      3 LVVF 6


RESULT 27
T13838
cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
C;Species: mitochondrion Bipes biporus
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13838
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: Z17789; MUID:97153826
A;Accession: T13838
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71335; NID:g1753232; PID:g1753235; PIDN:AAB48271.1
C;Genetics:
A;Genome: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 28
T13976
cytochrome-c oxidase (EC 1.9.3.1) chain I - Cnemidophorus tigris mitochondrion (fragment
C;Species: mitochondrion Cnemidophorus tigris
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13976
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangem
A;Reference number: Z17789; MUID:97153826
A;Accession: T13976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71332; NID:g1753236; PID:g1753239; PIDN:AAB48274.1
C;Genetics:
A;Genome: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 29
T17057
cytochrome-c oxidase (EC 1.9.3.1) chain I - Crotaphytus collaris mitochondrion (fragm
C;Species: mitochondrion Crotaphytus collaris
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17057
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial
A;Reference number: Z18674; MUID:97315309
A;Accession: T17057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82681; NID:g3603108; PID:g3603111; PIDN:AAC62272.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match             23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 30
T12303
cytochrome-c oxidase (EC 1.9.3.1) chain I - Dipsosaurus dorsalis mitochondrion (fragm
C;Species: mitochondrion Dipsosaurus dorsalis
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C;Accession: T12303
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example
A;Reference number: Z17488; MUID:99162288
A;Accession: T12303
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>
A;Cross-references: EMBL:AF049857; NID:g4105726; PID:g4105729; PIDN:AAD02514.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase
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  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 31
T14019
cytochrome-c oxidase (EC 1.9.3.1) chain I - Eremias grammica mitochondrion (fragment)
C;Species: mitochondrion Eremias grammica
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14019
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: Z17789; MUID:97153826
A;Accession: T14019
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71331; NID:g1753240; PID:g1753243; PIDN:AAB48277.1
C;Genetics:
A;Genome: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 32
T17060
cytochrome-c oxidase (EC 1.9.3.1) chain I - Gambelia wislizenii mitochondrion (fragment)
C;Species: mitochondrion Gambelia wislizenii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17060
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A;Reference number: Z18674; MUID:97315309
A;Accession: T17060
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82682; NID:g3603120; PID:g3603123; PIDN:AAC62281.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 33
T14043
cytochrome-c oxidase (EC 1.9.3.1) chain I - Lialis jicari mitochondrion (fragment)
C;Species: mitochondrion Lialis jicari
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14043
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangem
A;Reference number: Z17789; MUID:97153826
A;Accession: T14043
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71327; NID:g1753244; PID:g1753247; PIDN:AAB48280.1
C;Genetics:
A;Genome: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 34
T14054
cytochrome-c oxidase (EC 1.9.3.1) chain I - Mabuya aurata mitochondrion (fragment)
C;Species: mitochondrion Mabuya aurata
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14054
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangem
A;Reference number: Z17789; MUID:97153826
A;Accession: T14054
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71330; NID:g1753248; PID:g1753251; PIDN:AAB48283.1
C;Genetics:
A;Genome: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 35
T17066
cytochrome-c oxidase (EC 1.9.3.1) chain I - Oplurus cuvieri mitochondrion (fragment)
C;Species: mitochondrion Oplurus cuvieri
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17066
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial
A;Reference number: Z18674; MUID:97315309
A;Accession: T17066
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82685; NID:g3603136; PID:g3603139; PIDN:AAC62293.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase
```

```
  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 36
T17069
cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynosoma douglassii mitochondrion (fragmen
C;Species: mitochondrion Phrynosoma douglassii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17069
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A;Reference number: Z18674; MUID:97315309
A;Accession: T17069
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82686; NID:g3603144; PID:g3603147; PIDN:AAC62299.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 37
T12308
cytochrome-c oxidase (EC 1.9.3.1) chain I - Sator angustus mitochondrion (fragment)
C;Species: mitochondrion Sator angustus
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C;Accession: T12308
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usi
A;Reference number: Z17488; MUID:99162288
A;Accession: T12308
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>
A;Cross-references: EMBL:AF049859; NID:g4105734; PID:g4105737; PIDN:AAD02520.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 38
T17072
cytochrome-c oxidase (EC 1.9.3.1) chain I - Sauromalus obesus mitochondrion (fragment)
C;Species: mitochondrion Sauromalus obesus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17072
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial
A;Reference number: Z18674; MUID:97315309
A;Accession: T17072
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82687; NID:g3603152; PID:g3603155; PIDN:AAC62305.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 39
T12312
cytochrome-c oxidase (EC 1.9.3.1) chain I - Sceloporus graciosus mitochondrion (fragm
C;Species: mitochondrion Sceloporus graciosus
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C;Accession: T12312
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example
A;Reference number: Z17488; MUID:99162288
A;Accession: T12312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>
A;Cross-references: EMBL:AF049860; NID:g4105738; PID:g4105741; PIDN:AAD02523.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 40
T12316
cytochrome-c oxidase (EC 1.9.3.1) chain I - Uma scoparia mitochondrion (fragment)
C;Species: mitochondrion Uma scoparia
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C;Accession: T12316
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example
A;Reference number: Z17488; MUID:99162288
A;Accession: T12316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>
A;Cross-references: EMBL:AF049861; NID:g4105742; PID:g4105745; PIDN:AAD02526.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match           23.6%;  Score 13;  DB 2;  Length 10;
```

Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      7 FFA 9
          ||:
Db      7 FFS 9
```

RESULT 41
T12321
cytochrome-c oxidase (EC 1.9.3.1) chain I - Uta stansburiana mitochondrion (fragment)
C;Species: mitochondrion Uta stansburiana
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C;Accession: T12321
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usi
A;Reference number: Z17488; MUID:99162288
A;Accession: T12321
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>
A;Cross-references: EMBL:AF049863; NID:g4105750; PID:g4105753; PIDN:AAD02532.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      7 FFA 9
          ||:
Db      7 FFS 9
```

RESULT 42
T14219
cytochrome-c oxidase (EC 1.9.3.1) chain I - Xenosaurus grandis mitochondrion (fragment)
C;Species: mitochondrion Xenosaurus grandis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14219
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: Z17789; MUID:97153826
A;Accession: T14219
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71333; NID:g5739536; PIDN:AAC62821.1; PID:g1753275
C;Genetics:
A;Genome: mitochondrion
A;Note: CO1
C;Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      7 FFA 9
          ||:
Db      7 FFS 9
```

RESULT 43
JQ1273
neuropeptide Antho-KAamide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 08-Dec-1995
C;Accession: JQ1273
R;Nothacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991
A;Title: Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuro
A;Reference number: JQ1273; MUID:92028852
A;Accession: JQ1273
A;Molecule type: protein
A;Residues: 1-4 <NOT>
C;Comment: The carboxyl-terminal amide probably arises from cleavage of a following g
C;Keywords: amidated carboxyl end; neuropeptide; phenyllactylation
F;1/Modified site: L-3-phenyllactic acid (Phe) #status experimental
F;4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 21.8%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      7 FF 8
          ||
Db      1 FF 2
```

RESULT 44
A32480
achatin-I - giant African snail
N;Contains: achatin-II
C;Species: Achatina fulica (giant African snail)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
C;Accession: A32480
R;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.;
Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica f
A;Reference number: A32480; MUID:89273551
A;Accession: A32480
A;Molecule type: protein
A;Residues: 1-4 <KAM>
A;Note: stereochemistry of the active form confirmed by chemical synthesis
R;Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nom
FEBS Lett. 307, 253-256, 1992
A;Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous ne
(H-Gly-Phe-Ala-Asp-OH).
A;Reference number: A44691; MUID:92354723
A;Contents: annotation; X-ray crystallography, 0.85 angstroms
A;Note: achatin-II has L-phenylalanine
C;Keywords: D-amino acid
F;2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 21.8%; Score 12; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      8 FAE 10
          ||:
Db      2 FAD 4
```

RESULT 45
A60986
N-formyl oligopeptide - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Accession: A60986
R;Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A;Title: Purification and amino acid sequencing of naturally occurring N-formyl-methi
A;Reference number: A60986; MUID:90092408
A;Accession: A60986
A;Molecule type: protein
A;Residues: 1-6 <BRO>
C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reporte
F;1/Modified site: N-formylmethionine #status experimental

Query Match 21.8%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      5 LVF 7
          :||
Db      1 MVF 3


RESULT 46
I59142
platelet-derived growth factor B chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I59142
R;Pech, M.; Gazit, A.; Arnstein, P.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 2693-2697, 1989
A;Title: Generation of fibrosarcomas in vivo by a retrovirus that expressed the normal B
A;Reference number: I59142; MUID:89202393
A;Accession: I59142
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:M26180; NID:g516624; PIDN:AAA39905.1; PID:g516625

  Query Match             21.8%;  Score 12;  DB 2;  Length 6;
  Best Local Similarity   66.7%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVF 7
          :||
Db      1 MVF 3


RESULT 47
A43129
neuropeptide GNFFRFamide - tapeworm (Moniezia expansa)
C;Species: Moniezia expansa
C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997
C;Accession: A43129
R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
A;Title: GNFFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t
A;Reference number: A43129; MUID:93312289
A;Accession: A43129
A;Molecule type: protein
A;Residues: 1-6 <MAU>
C;Keywords: amidated carboxyl end; neuropeptide
F;6/Modified site: amidated carboxyl end (Phe) #status predicted

  Query Match             21.8%;  Score 12;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      3 FF 4


RESULT 48
PT0246
Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0246
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0246
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

  Query Match             21.8%;  Score 12;  DB 2;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKL 5
          |: |
Db      1 HEVL 4


RESULT 49
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventric
A;Reference number: I46868; MUID:84221901
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

  Query Match             21.8%;  Score 12;  DB 2;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 QKL 5
          ||:
Db      1 QKM 3


RESULT 50
T13818
cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T13818
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the
A;Reference number: Z17775; MUID:97398704
A;Accession: T13818
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DEL>
A;Cross-references: EMBL:Y09527; NID:g2340019; PIDN:CAA70718.1; PID:g2340022
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion

  Query Match             21.8%;  Score 12;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      7 FF 8


Search completed: October 29, 2002, 09:38:49
Job time : 15 secs
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:31:37 ; Search time 11 Seconds
(without alignments)
35.200 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 349

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	32.7	10	1	COXM_RAT	P80431 rattus norv
2	16	29.1	5	1	RE11_LITRU	P82070 litoria rub
3	16	29.1	5	1	RE21_LITRU	P82071 litoria rub
4	16	29.1	10	1	PAP1_PARMA	P81863 pardachirus
5	15	27.3	5	1	UC22_MAIZE	P80628 zea mays (m
6	15	27.3	7	1	FAR2_ASCSU	P31890 ascaris suu
7	15	27.3	10	1	RCA_PINPS	P81084 pinus pinas
8	14	25.5	7	1	CCF1_ENTFA	P20104 enterococcu
9	14	25.5	8	1	CPD1_ENTFA	P13269 enterococcu
10	14	25.5	9	1	SAMP_MUSCA	P19095 mustelus ca
11	14	25.5	10	1	COXK_ONCMY	P80332 oncorhynchu
12	13	23.6	8	1	UPAA_HUMAN	P30096 homo sapien
13	13	23.6	10	1	COXA_ONCMY	P80328 oncorhynchu
14	13	23.6	10	1	COXO_RAT	P80432 rattus norv
15	12	21.8	4	1	ACH1_ACHFU	P35904 achatina fu
16	12	21.8	4	1	FFKA_ANTEL	P58705 anthopleura
17	12	21.8	5	1	PAP2_PARMA	P81864 pardachirus
18	12	21.8	5	1	RE31_LITRU	P82072 litoria rub
19	12	21.8	5	1	RE32_LITRU	P82073 litoria rub
20	12	21.8	6	1	FARP_MONEX	P41966 moniezia ex
21	12	21.8	8	1	B44K_PORGI	P81886 porphyromon
22	12	21.8	9	1	FIBB_ERYPA	P19346 erythrocebu
23	12	21.8	10	1	COXO_THUOB	P80982 thunnus obe
24	12	21.8	10	1	FARP_MANSE	P18523 manduca sex
25	12	21.8	10	1	FARP_MYTED	P42560 mytilus edu
26	12	21.8	10	1	FIBB_CERSI	P14537 ceratotheri
27	12	21.8	10	1	MOSQ_CLYJA	P19962 clypeaster
28	12	21.8	10	1	TKNK_PIG	P01292 sus scrofa
29	12	21.8	10	1	TKU2_UREUN	P40752 urechis uni
30	12	21.8	10	1	TPIS_NICPL	P19118 nicotiana p
31	12	21.8	10	1	TRP6_LEUMA	P81738 leucophaea
32	12	21.8	10	1	TRP7_LEUMA	P81739 leucophaea
33	11	20.0	7	1	CHOX_ALCSP	P16101 alcaligenes
34	11	20.0	7	1	HY7_PIG	P01153 sus scrofa
35	11	20.0	7	1	UF03_MOUSE	P38641 mus musculu
36	11	20.0	8	1	AKH_TABAT	P14595 tabanus atr
37	11	20.0	8	1	HTF2_PERAM	P04549 periplaneta
38	11	20.0	9	1	FAR5_PANRE	P82661 panagrellus
39	11	20.0	9	1	ULAK_MOUSE	P99031 mus musculu
40	11	20.0	10	1	BPP2_BOTIN	P30422 bothrops in
41	11	20.0	10	1	FAR6_PANRE	P82660 panagrellus
42	11	20.0	10	1	GON1_PETMA	P04378 petromyzon
43	11	20.0	10	1	HTF2_CARMO	P11385 carausius m
44	11	20.0	10	1	HTF_HELZE	P16353 heliothis z
45	11	20.0	10	1	HTF_TABAT	P14596 tabanus atr
46	11	20.0	10	1	Q2OB_COMTE	P80465 comamonas t
47	10	18.2	5	1	BPP7_BOTIN	P30425 bothrops in
48	10	18.2	8	1	ACI_THUAL	P18691 thunnus alb
49	10	18.2	8	1	ALL1_CYDPO	P82152 cydia pomon
50	10	18.2	8	1	LCK8_LEUMA	P19990 leucophaea

ALIGNMENTS

RESULT 1
COXM_RAT
ID COXM_RAT STANDARD; PRT; 10 AA.
AC P80431;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=WISTAR; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 32.7%; Score 18; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 HQK 4
          |||
Db      2 HQK 4
```

RESULT 2
RE11_LITRU
ID RE11_LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  598 MW;  6DD9C9CAB2A00000 CRC64;

  Query Match             29.1%;  Score 16;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          |||
Db      3 FFA 5


RESULT 3
RE21_LITRU
ID   RE21_LITRU     STANDARD;      PRT;     5 AA.
AC   P82071;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  626 MW;  6DD9C9CB10300000 CRC64;

  Query Match             29.1%;  Score 16;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          |||
Db      3 FFA 5


RESULT 4
PAP1_PARMA
ID   PAP1_PARMA     STANDARD;      PRT;     10 AA.
AC   P81863;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pardaxin I (PXI) (Fragment).
OS   Pardachirus marmoratus (Red sea moses sole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Soleoidei; Soleidae; Pardachirus.
OX   NCBI_TaxID=31087;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC       PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN
CC       MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS. SHOWN
CC       TO BE 5-10 TIMES MORE TOXIC, CYTOLYTIC AND ACTIVE IN MEMBRANE PORE
CC       FORMATION THAN PARDAXIN II.
CC   -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW   Toxin.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1063 MW;  D399C36760572DD9 CRC64;

  Query Match             29.1%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          |||
Db      2 FFA 4


RESULT 5
UC22_MAIZE
ID   UC22_MAIZE     STANDARD;      PRT;     5 AA.
AC   P80628;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE   (Fragment).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Coleoptile;
RA   Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA   Pernollet J.-C., Zivy M., de Vienne D.;
RT   "The maize two dimensional gel protein database: towards an integrated
RT   genome analysis program.";
RL   Theor. Appl. Genet. 93:997-1005(1996).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR   Maize-2DPAGE; P80628; COLEOPTILE.
DR   MaizeDB; 123954; -.
FT   NON_TER       1      1
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  654 MW;  72CB19C9C0300000 CRC64;

  Query Match             27.3%;  Score 15;  DB 1;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 VFF 8
          :||
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Db      1 IFF 3


RESULT 6
FAR2_ASCSU
ID   FAR2_ASCSU     STANDARD;      PRT;     7 AA.
AC   P31890;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   FMRFamide-like neuropeptide AF2.
OS   Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
OS   Panagrellus redivivus.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC   Ascarididae; Ascaris.
OX   NCBI_TaxID=6253, 6233;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=A.suum;
RX   MEDLINE=93324431; PubMed=8332542;
RA   Cowden C., Stretton A.O.W.;
RT   "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
RL   Peptides 14:423-430(1993).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.redivivus;
RX   MEDLINE=95060998; PubMed=7970891;
RA   Maule A.G., Shaw C., Bowman J.W.;
RT   "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the
RT   free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";
RL   Parasitology 109:351-356(1994).
CC   -!- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
CC   -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
CC       GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  992 MW;  69D4073B5B11E350 CRC64;

  Query Match             27.3%;  Score 15;  DB 1;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 HQKLVF 7
          |: | |
Db      2 HEYLRF 7


RESULT 7
RCA_PINPS
ID   RCA_PINPS      STANDARD;      PRT;     10 AA.
AC   P81084;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable ribulose bisphosphate carboxylase/oxygenase activase (RuBisCO
DE   activase) (RA) (Water stress responsive protein 4) (Fragment).
OS   Pinus pinaster (Maritime pine).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX   NCBI_TaxID=71647;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Needle;
RX   MEDLINE=98418576; PubMed=9747804;
RA   Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT   "Water-deficit-responsive proteins in maritime pine.";
RL   Plant Mol. Biol. 38:587-596(1998).
RN   [2]
RP   SEQUENCE.
RC   TISSUE=Needle;
RX   MEDLINE=99274088; PubMed=10344291;
RA   Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA   Frigerio J.-M., Plomion C.;
RT   "Separation and characterization of needle and xylem maritime pine
RT   proteins.";
RL   Electrophoresis 20:1098-1108(1999).
CC   -!- FUNCTION: ACTIVATION OF RUBISCO (RIBULOSE-1,5-BISPHOSPHATE
CC       CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CC       CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC       CARBAMATE STRUCTURE (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC   -!- INDUCTION: BY WATER STRESS.
CC   -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW   Chloroplast; ATP-binding.
FT   NON_TER       1       1
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1171 MW;  C0A506D2C72B1EA6 CRC64;

  Query Match             27.3%;  Score 15;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 2.9e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVF 7
          :|||
Db      5 ELVF 8


RESULT 8
CCF1_ENTFA
ID   CCF1_ENTFA     STANDARD;      PRT;     7 AA.
AC   P20104;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Last annotation update)
DE   Sex pheromone CCF10.
OS   Enterococcus faecalis (Streptococcus faecalis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC   Enterococcus.
OX   NCBI_TaxID=1351;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=89008313; PubMed=3139658;
RA   Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA   Adsit J.C., Dunny G.M., Suzuki A.;
RT   "Structure of cCF10, a peptide sex pheromone which induces
RT   conjugative transfer of the Streptococcus faecalis tetracycline
RT   resistance plasmid, pCF10.";
RL   J. Biol. Chem. 263:14574-14578(1988).
CC   -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC       HEMOLYSIN PLASMID PCF10.
DR   PIR; A30812; A30812.
KW   Pheromone.
SQ   SEQUENCE   7 AA;  790 MW;  72C9D2C731B2C740 CRC64;

  Query Match             25.5%;  Score 14;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVF 7
          |||
Db      4 LVF 6


RESULT 9
CPD1_ENTFA
ID   CPD1_ENTFA     STANDARD;      PRT;     8 AA.
AC   P13269;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Last annotation update)
DE   Sex pheromone CPD1.
OS   Enterococcus faecalis (Streptococcus faecalis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC   Enterococcus.
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OX   NCBI_TaxID=1351;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85040388; PubMed=6436978;
RA   Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA   Craig R.A., Clewell D.B.;
RT   "Isolation and structure of bacterial sex pheromone, cPD1.";
RL   Science 226:849-850(1984).
CC   -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC       BACTERIOCIN PLASMID PPD1.
KW   Pheromone.
SQ   SEQUENCE   8 AA;  913 MW;  8665B729C682C729 CRC64;

  Query Match             25.5%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          || |
Db      2 LVMF 5


RESULT 10
SAMP_MUSCA
ID   SAMP_MUSCA     STANDARD;      PRT;     9 AA.
AC   P19095;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serum amyloid P-component (SAP) (Fragment).
OS   Mustelus canis (Smooth dogfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC   Mustelus.
OX   NCBI_TaxID=7812;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83160932; PubMed=6403520;
RA   Robey F.A., Tanaka T., Liu T.-Y.;
RT   "Isolation and characterization of two major serum proteins from the
RT   dogfish, Mustelus canis, C-reactive protein and amyloid P
RT   component.";
RL   J. Biol. Chem. 258:3889-3894(1983).
CC   -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC       ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC   -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC       IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC   -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR   PIR; B20569; B20569.
DR   InterPro; IPR001759; Pentaxin.
DR   PROSITE; PS00289; PENTAXIN; PARTIAL.
KW   Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT   DOMAIN        1      >9       PENTAXIN.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  965 MW;  D05B5735B3386769 CRC64;

  Query Match             25.5%;  Score 14;  DB 1;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 QKLVF 7
            : |:|
Db      5 KSLIF 9


RESULT 11
COXK_ONCMY
ID   COXK_ONCMY     STANDARD;      PRT;     10 AA.
AC   P80332;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIIa-heart (EC 1.9.3.1) (Fragment).
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=94237150; PubMed=8181469;
RA   Freund R., Kadenbach B.;
RT   "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT   of cytochrome c oxidase isolated from rainbow trout.";
RL   Eur. J. Biochem. 221:1111-1116(1994).
CC   -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC       CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC       MITOCHONDRIAL ELECTRON TRANSPORT.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR   PIR; S43631; S43631.
KW   Oxidoreductase; Inner membrane; Mitochondrion.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1174 MW;  4C8D81CAFAF772C3 CRC64;

  Query Match             25.5%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 QKL 5
          |||
Db      8 QKL 10


RESULT 12
UPAA_HUMAN
ID   UPAA_HUMAN     STANDARD;      PRT;     8 AA.
AC   P30096;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=93092937; PubMed=1459097;
RA   Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA   Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA   Hochstrasser D.F.;
RT   "Plasma protein map: an update by microsequencing.";
RL   Electrophoresis 13:707-714(1992).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR   SWISS-2DPAGE; P30096; HUMAN.
FT   NON_TER       1      1
FT   VARIANT       5      5       F -> P.
FT                                /FTId=VAR_000004.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  909 MW;  86677B59D1A72042 CRC64;

  Query Match             23.6%;  Score 13;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          | |:
Db      3 LTFY 6
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RESULT 13
COXA_ONCMY
ID   COXA_ONCMY     STANDARD;      PRT;    10 AA.
AC   P80328;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cytochrome c oxidase polypeptide VA (EC 1.9.3.1) (Fragment).
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=94237150; PubMed=8181469;
RA   Freund R., Kadenbach B.;
RT   "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT   of cytochrome c oxidase isolated from rainbow trout.";
RL   Eur. J. Biochem. 221:1111-1116(1994).
CC   -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC       OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR   PIR; S43625; S43625.
KW   Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT   NON_TER       10      10
SQ   SEQUENCE   10 AA;  1144 MW;  C535C5B1AB02C33D CRC64;

  Query Match             23.6%;  Score 13;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 7e+03;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 HQKL 5
           | |:
Db       2 HAKV 5


RESULT 14
COXO_RAT
ID   COXO_RAT       STANDARD;      PRT;    10 AA.
AC   P80432;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIIc, mitochondrial (EC 1.9.3.1)
DE   (VIIIA) (Fragment).
GN   COX7C OR COX7C1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=WISTAR; TISSUE=Liver, and Heart;
RX   MEDLINE=95324529; PubMed=7601105;
RA   Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT   "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT   amino-terminal sequences suggest identity of the fetal heart and the
RT   adult liver isoform.";
RL   Eur. J. Biochem. 230:235-241(1995).
CC   -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC       CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC       MITOCHONDRIAL ELECTRON TRANSPORT.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW   Oxidoreductase; Mitochondrion.
FT   NON_TER       10      10
SQ   SEQUENCE   10 AA;  1117 MW;  126DE767687B1B0B CRC64;

  Query Match             23.6%;  Score 13;  DB 1;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 7e+03;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQK 4
           |:::
Db       2 HYEE 5


RESULT 15
ACH1_ACHFU
ID   ACH1_ACHFU     STANDARD;      PRT;     4 AA.
AC   P35904;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Achatin-I.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Achatinacea; Achatinidae; Achatina.
OX   NCBI_TaxID=6530;
RN   [1]
RP   SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC   STRAIN=FERUSSAC; TISSUE=Ganglion;
RX   MEDLINE=89273551; PubMed=2597281;
RA   Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA   Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA   Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT   "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT   fulica Ferussac containing a D-amino acid residue.";
RL   Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN   [2]
RP   CHARACTERIZATION.
RC   STRAIN=FERUSSAC; TISSUE=Heart atrium;
RX   MEDLINE=91264856; PubMed=1675568;
RA   Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA   Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT   "Purification of achatin-I from the atria of the African giant snail,
RT   Achatina fulica, and its possible function.";
RL   Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=93014529; PubMed=1399265;
RA   Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA   Iwashita T., Nomoto K.;
RT   "Crystal structure and molecular conformation of achatin-I
RT   (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT   D-amino acid residue.";
RL   Int. J. Pept. Protein Res. 39:258-264(1992).
CC   -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC       AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC       NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC       HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR   PIR; A32480; A32480.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-PHENYLALANINE.
SQ   SEQUENCE   4 AA;  408 MW;  6AADD9C810000000 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       8 FAE 10
           ||:
Db       2 FAD 4


RESULT 16
FFKA_ANTEL
ID   FFKA_ANTEL     STANDARD;      PRT;     4 AA.
AC   P58705;
DT   01-MAR-2002 (Rel. 41, Created)
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DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Antho-KAamide.
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE.
RX   PubMed=1681803;
RA   Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT   "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
RT   novel neuropeptide from sea anemones.";
RL   Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN   [2]
RP   FUNCTION.
RX   PubMed=8397415;
RA   McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT   "The expansion behaviour of sea anemones may be coordinated by two
RT   inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC   -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC       groups. May be involved in the expansion phase of feeding
CC       behaviour in sea anemones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron-specific.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1       1       L-3-PHENYLLACTYL.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  512 MW;  6DD339C9A0000000 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      1 FF 2


RESULT 17
PAP2_PARMA
ID   PAP2_PARMA     STANDARD;      PRT;     5 AA.
AC   P81864;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pardaxin II (PXII) (Fragment).
OS   Pardachirus marmoratus (Red sea moses sole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Soleoidei; Soleidae; Pardachirus.
OX   NCBI_TaxID=31087;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC       PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC       IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC   -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW   Toxin.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  614 MW;  7769C9C9C8100000 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      2 FF 3


RESULT 18
RE31_LITRU
ID   RE31_LITRU     STANDARD;      PRT;     5 AA.
AC   P82072;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  656 MW;  71A9C9CB10300000 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      3 FF 4


RESULT 19
RE32_LITRU
ID   RE32_LITRU     STANDARD;      PRT;     5 AA.
AC   P82073;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 3.2.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW   Amphibian skin.
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SQ   SEQUENCE   5 AA;  570 MW;  71A9C9C862A00000 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      3 FF 4


RESULT 20
FARP_MONEX
ID   FARP_MONEX     STANDARD;      PRT;     6 AA.
AC   P41966;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   FMRFamide-like neuropeptide GNFFRF-amide.
OS   Moniezia expansa (Sheep tapeworm).
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC   Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
OC   Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Anoplocephalidae;
OC   Moniezia.
OX   NCBI_TaxID=28841;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93312289; PubMed=8323531;
RA   Maule A.G., Shaw C., Halton D.W., Thim L.;
RT   "GNFFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
RT   the sheep tapeworm, Moniezia expansa.";
RL   Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       6       6       AMIDATION.
SQ   SEQUENCE   6 AA;  787 MW;  69D409C9C4481000 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      3 FF 4


RESULT 21
B44K_PORGI
ID   B44K_PORGI     STANDARD;      PRT;     8 AA.
AC   P81886;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   44 kDa immunogenic protein (Fragment).
OS   Porphyromonas gingivalis (Bacteroides gingivalis).
OC   Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
OC   Porphyromonas.
OX   NCBI_TaxID=837;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=VPB 3492;
RX   MEDLINE=20198497; PubMed=10731616;
RA   Norris J.M., Love D.N.;
RT   "Serum antibody responses of cats to soluble whole cell antigens of
RT   feline Porphyromonas gingivalis.";
RL   Vet. Microbiol. 73:37-49(2000).
CC   -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW   Antigen.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  989 MW;  9554540326CB476D CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQK 4
          :||
Db      3 YQK 5


RESULT 22
FIBB_ERYPA
ID   FIBB_ERYPA     STANDARD;      PRT;     9 AA.
AC   P19346;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN   FGB.
OS   Erythrocebus patas (Red guenon) (Hussar).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Erythrocebus.
OX   NCBI_TaxID=9538;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85289140; PubMed=3928610;
RA   Nakamura S., Takenaka O., Takahashi K.;
RT   "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT   patas monkey (Erythrocebus patas): their amino acid sequences,
RT   restricted mutations, and a molecular phylogeny for macaques,
RT   guenons, and baboons.";
RL   J. Biochem. 97:1487-1492(1985).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR   PIR; D24180; D24180.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1       9       FIBRINOPEPTIDE B.
FT   NON_TER       9       9
SQ   SEQUENCE   9 AA;  1020 MW;  69FE7879C732CB1B CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 9;
  Best Local Similarity   16.7%;  Pred. No. 1e+05;
  Matches    1;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQKLVF 7
          :::::|
Db      1 NEEVLF 6


RESULT 23
COXO_THUOB
ID   COXO_THUOB     STANDARD;      PRT;    10 AA.
AC   P80982;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIIc (EC 1.9.3.1) (Fragment).
OS   Thunnus obesus (Bigeye tuna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8241;
RN   [1]
RP   SEQUENCE.
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RC   TISSUE=Heart, and Liver;
RX   MEDLINE=97454291; PubMed=9310366;
RA   Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA   Kadenbach B.;
RT   "The subunit structure of cytochrome-c oxidase from tuna heart and
RT   liver.";
RL   Eur. J. Biochem. 248:99-103(1997).
CC   -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC       CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC       MITOCHONDRIAL ELECTRON TRANSPORT.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW   Oxidoreductase; Inner membrane; Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1059 MW;  126DE767687B1DCB CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       8 FAE 10
           :||
Db       3 YAE 5


RESULT 24
FARP_MANSE
ID   FARP_MANSE     STANDARD;      PRT;    10 AA.
AC   P18523;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide.
OS   Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Sphingiodea; Sphingidae; Sphinginae; Manduca.
OX   NCBI_TaxID=7130;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91045350; PubMed=2235684;
RA   Kingan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
RA   Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
RA   Hunt D.F.;
RT   "A new peptide in the FMRFamide family isolated from the CNS of the
RT   hawkmoth, Manduca sexta.";
RL   Peptides 11:849-856(1990).
CC   -!- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
CC       THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
CC       MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
CC       FLIGHT BEHAVIOR PATTERNS.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
DR   PIR; A43977; A43977.
KW   Amidation; Neuropeptide.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1247 MW;  D3C45229D5B1F2D2 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 HQKLVF 7
           |  | |
Db       5 HSFLRF 10


RESULT 25
FARP_MYTED
ID   FARP_MYTED     STANDARD;      PRT;    10 AA.
AC   P42560;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   FMRFamide-like neuropeptide ALAGDHFFRF-amide.
OS   Mytilus edulis (Blue mussel).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC   Mytiloidea; Mytilidae; Mytilus.
OX   NCBI_TaxID=6550;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93047883; PubMed=1358534;
RA   Walker R.J.;
RT   "Neuroactive peptides with an RFamide or Famide carboxyl terminal.";
RL   Comp. Biochem. Physiol. 102C:213-222(1992).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1180 MW;  C2F80CC9C1EAA87D CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FF 8
           ||
Db       7 FF 8


RESULT 26
FIBB_CERSI
ID   FIBB_CERSI     STANDARD;      PRT;    10 AA.
AC   P14537;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN   FGB.
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX   NCBI_TaxID=9807;
RN   [1]
RP   SEQUENCE.
RA   O'Neil P.B., Doolittle R.F.;
RT   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL   Syst. Zool. 22:590-595(1973).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     10       FIBRINOPEPTIDE B.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1097 MW;  9402B2B2CDDDD33A CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQK 4
           |  |
Db       1 HDDK 4
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RESULT 27
MOSQ_CLYJA
ID   MOSQ_CLYJA     STANDARD;      PRT;    10 AA.
AC   P19962;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Last annotation update)
DE   [Gln-6]-mosact.
OS   Clypeaster japonicus (Sand dollar).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroida;
OC   Clypeasteridae; Clypeaster.
OX   NCBI_TaxID=7644;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Egg jelly;
RA   Suzuki N., Kurita M., Yoshino K., Kajiura H., Nomura K., Yamaguchi M.;
RT   "Purification and structure of mosact and its derivatives from the
RT   egg jelly of the sea urchin Clypeaster japonicus.";
RL   Zool. Sci. 4:649-656(1987).
CC   -!- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
DR   PIR; JN0025; JN0025.
SQ   SEQUENCE   10 AA;  1019 MW;  9AFB032456DDC5BA CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 QKLV 6
           | |:
Db       6 QNLI 9


RESULT 28
TKNK_PIG
ID   TKNK_PIG       STANDARD;      PRT;    10 AA.
AC   P01292;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Neurokinin B (NKB) (Neuromedin K).
GN   TAC3 OR NKNB.
OS   Sus scrofa (Pig), and
OS   Rana ridibunda (Laughing frog) (Marsh frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823, 8406;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Pig; TISSUE=Spinal cord;
RX   MEDLINE=83282812; PubMed=6576785;
RA   Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT   "Neuromedin K: a novel mammalian tachykinin identified in porcine
RT   spinal cord.";
RL   Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=R.ridibunda; TISSUE=Brain;
RX   MEDLINE=92044543; PubMed=1658233;
RA   O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT   "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT   neurokinin B from the brain of the frog Rana ridibunda.";
RL   J. Neurochem. 57:2086-2091(1991).
CC   -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC       EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC       SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC       MUSCLES.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR   PIR; A01560; SPPGNK.
DR   InterPro; IPR002040; Tachykinin.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1211 MW;  E1FA7C62C9C9CAA1 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FF 8
             ||
Db       5 FF 6


RESULT 29
TKU2_UREUN
ID   TKU2_UREUN     STANDARD;      PRT;    10 AA.
AC   P40752;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Urechistachykinin II.
OS   Urechis unicinctus.
OC   Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
OX   NCBI_TaxID=6432;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Ventral nerve cord;
RX   MEDLINE=93236558; PubMed=8476410;
RA   Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;
RT   "Two novel tachykinin-related neuropeptides in the echiuroid worm,
RT   Urechis unicinctus.";
RL   Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC   -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
CC       MUSCLE OF THE ANIMAL.
CC   -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  984 MW;  3F58DD79C9C87698 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FF 8
             ||
Db       6 FF 7


RESULT 30
TPIS_NICPL
ID   TPIS_NICPL     STANDARD;      PRT;    10 AA.
AC   P19118;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS   Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4092;
RN   [1]
RP   SEQUENCE.
RA   Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT   "Alterations in the phenotype of plant cells studied by NH2-terminal
RT   amino acid-sequence analysis of proteins electroblotted from two-
RT   dimensional gel-separated total extracts.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC       phosphate.
CC   -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
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CC       AND PLASTID.
CC   -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR   PIR; A27617; A27617.
DR   InterPro; IPR000652; Trioseph_isomerase.
DR   Pfam; PF00121; TIM; 1.
DR   PROSITE; PS00171; TIM; PARTIAL.
KW   Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW   Pentose shunt.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1140 MW;  80B9D37862C9C9D1 CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      4 FF 5


RESULT 31
TRP6_LEUMA
ID   TRP6_LEUMA     STANDARD;      PRT;     10 AA.
AC   P81738;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Tachykinin-related peptide 6 (LemTRP 6).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blaberoidea; Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Brain;
RX   MEDLINE=97269266; PubMed=9114447;
RA   Muren J.E., Naessel D.R.;
RT   "Seven tachykinin-related peptides isolated from the brain of the
RT   madeira cockroach; evidence for tissue-specific expression of
RT   isoforms.";
RL   Peptides 18:7-15(1997).
CC   -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC       OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC   -!- TISSUE SPECIFICITY: BRAIN.
CC   -!- MASS SPECTROMETRY: MW=1023.0; METHOD=MALDI.
CC   -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1024 MW;  C4469D79C9C87DDD CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      6 FF 7


RESULT 32
TRP7_LEUMA
ID   TRP7_LEUMA     STANDARD;      PRT;     10 AA.
AC   P81739;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Tachykinin-related peptide 7 (LemTRP 7).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blaberoidea; Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Brain;
RX   MEDLINE=97269266; PubMed=9114447;
RA   Muren J.E., Naessel D.R.;
RT   "Seven tachykinin-related peptides isolated from the brain of the
RT   madeira cockroach; evidence for tissue-specific expression of
RT   isoforms.";
RL   Peptides 18:7-15(1997).
CC   -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC       OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC   -!- TISSUE SPECIFICITY: BRAIN.
CC   -!- MASS SPECTROMETRY: MW=1069.7; METHOD=MALDI.
CC   -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1068 MW;  C4541679C9C865BD CRC64;

  Query Match             21.8%;  Score 12;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FF 8
          ||
Db      6 FF 7


RESULT 33
CHOX_ALCSP
ID   CHOX_ALCSP     STANDARD;      PRT;     7 AA.
AC   P16101;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-APR-1990 (Rel. 14, Last annotation update)
DE   Choline oxidase (EC 1.1.3.17) (Fragment).
OS   Alcaligenes sp.
OC   Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC   Alcaligenes.
OX   NCBI_TaxID=512;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81006769; PubMed=6997283;
RA   Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT   "Identification and properties of the prosthetic group of choline
RT   oxidase from Alcaligenes sp.";
RL   J. Biochem. 88:197-203(1980).
CC   -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR   PIR; A15398; A15398.
KW   Oxidoreductase.
FT   NON_TER      7      7
SQ   SEQUENCE   7 AA;  839 MW;  7415B1E457644AC0 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HHQK 4
          :| :
Db      4 NHSR 7


RESULT 34
HY7_PIG
ID   HY7_PIG        STANDARD;      PRT;     7 AA.
AC   P01153;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   Hypothalamic heptapeptide.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
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RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RX   MEDLINE=81213980; PubMed=6263778;
RA   Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA   Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT   "Isolation, structure and synthesis of a heptapeptide with in vitro
RT   ACTH-releasing activity from porcine hypothalamus.";
RL   Horm. Metab. Res. 13:228-232(1981).
DR   PIR; A01417; NYPG7.
SQ   SEQUENCE   7 AA;  957 MW;  632B45B1FB5059A0 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HHQK 4
           |  |
Db       4 HSYK 7


RESULT 35
UF03_MOUSE
ID   UF03_MOUSE     STANDARD;      PRT;     7 AA.
AC   P38641;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins
RT   using preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
FT   NON_TER       7       7
SQ   SEQUENCE   7 AA;  842 MW;  6AA72B1DDB1B1180 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 7;
  Best Local Similarity   33.3%;  Pred. No. 1e+05;
  Matches    1;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQK 4
           |::
Db       1 HEE 3


RESULT 36
AKH_TABAT
ID   AKH_TABAT      STANDARD;      PRT;     8 AA.
AC   P14595;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE   (DCC I).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC   Tabanidae; Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A33995; A33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  949 MW;  86786771A9D1A736 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 KLVF 7
           :| |
Db       1 QLTF 4


RESULT 37
HTF2_PERAM
ID   HTF2_PERAM     STANDARD;      PRT;     8 AA.
AC   P04549;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE   (PeA-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
OS   Periplaneta americana (American cockroach),
OS   Leptinotarsa decemlineata (Colorado potato beetle), and
OS   Blatta orientalis (Oriental cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978, 7539, 6976;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=85046530; PubMed=6548628;
RA   Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA   Rinehart K.L. Jr.;
RT   "Structures of two cockroach neuropeptides assigned by fast atom
RT   bombardment mass spectrometry.";
RL   Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=84298179; PubMed=6591205;
RA   Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA   Miller C.A., Schooley D.A.;
RT   "Isolation and primary structure of two peptides with
RT   cardioacceleratory and hyperglycemic activity from the corpora
RT   cardiaca of Periplaneta americana.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX   MEDLINE=90160053; PubMed=2576128;
RA   Gaede G., Kellner R.;
RT   "The metabolic neuropeptides of the corpus cardiacum from the potato
RT   beetle and the American cockroach are identical.";
RL   Peptides 10:1287-1289(1989).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
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RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A05170; A05170.
DR   PIR; S08996; S08996.
DR   PIR; B44960; B44960.
DR   PIR; B49823; B49823.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  1006 MW;  86745771A9D1A736 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 KLVF 7
          :| |
Db      1 QLTF 4


RESULT 38
FAR5_PANRE
ID   FAR5_PANRE     STANDARD;      PRT;     9 AA.
AC   P82661;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   FMRFamide-like neuropeptide PF5 (AMRNALVRF-amide).
OS   Panagrellus redivivus.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC   Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX   NCBI_TaxID=6233;
RN   [1]
RP   SEQUENCE, FUNCTION, AND AMIDATION.
RA   Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA   Maule A.G.;
RT   "Isolation, characterization and pharmacology of FMRFamide-related
RT   peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";
RL   Submitted (JUL-2000) to the SWISS-PROT data bank.
CC   -!- FUNCTION: MYOACTIVE.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       9      9       AMIDATION.
SQ   SEQUENCE   9 AA;  1077 MW;  A0D112C72DD45406 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          || |
Db      6 LVRF 9


RESULT 39
ULAK_MOUSE
ID   ULAK_MOUSE     STANDARD;      PRT;     9 AA.
AC   P99031;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RA   Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
RA   Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA   Cowthorne M.;
RL   Submitted (AUG-1998) to the SWISS-PROT data bank.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.
DR   SWISS-2DPAGE; P99031; MOUSE.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1106 MW;  E1E842C3240B145A CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 9;
  Best Local Similarity   16.7%;  Pred. No. 1e+05;
  Matches    1;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HHQKLV 6
            : :|::
Db      3 NERKVI 8


RESULT 40
BPP2_BOTIN
ID   BPP2_BOTIN     STANDARD;      PRT;     10 AA.
AC   P30422;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE   enzyme inhibitor).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8723;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC       ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC       BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC       IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR   PIR; B37196; B37196.
KW   Hypotensive agent; Venom.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   10 AA;  1213 MW;  30C53546C761F773 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HHQ 3
          | |
Db      5 HPQ 7


RESULT 41
FAR6_PANRE
ID   FAR6_PANRE     STANDARD;      PRT;     10 AA.
AC   P82660;
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DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS   Panagrellus redivivus.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC   Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX   NCBI_TaxID=6233;
RN   [1]
RP   SEQUENCE, FUNCTION, AND AMIDATION.
RA   Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA   Maule A.G.;
RT   "Isolation, characterization and pharmacology of RMRFamide-related
RT   peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";
RL   Submitted (JUL-2000) to the SWISS-PROT data bank.
CC   -!- FUNCTION: MYOACTIVE.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1132 MW;  CB13E4C9D776C76D CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    3;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 QKLVFF 8
           |  |.|
Db       5 QPFVRF 10


RESULT 42
GON1_PETMA
ID   GON1_PETMA     STANDARD;      PRT;    10 AA.
AC   P04378;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
DE   (Luliberin I).
OS   Petromyzon marinus (Sea lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Petromyzon.
OX   NCBI_TaxID=7757;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=86168192; PubMed=3514603;
RA   Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT   "Primary structure of gonadotropin-releasing hormone from lamprey
RT   brain.";
RL   J. Biol. Chem. 261:4812-4819(1986).
CC   -!- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
CC       FOLLICLE-STIMULATING HORMONES.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR   PIR; A01412; RHLMGS.
DR   InterPro; IPR002012; GnRH.
DR   Pfam; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Hormone; Amidation; Hypothalamus.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1244 MW;  1E4B36237B1735AB CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 HQKL 5
           |  |
Db       2 HYSL 5


RESULT 43
HTF2_CARMO
ID   HTF2_CARMO     STANDARD;      PRT;    10 AA.
AC   P11385;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
DE   neuropeptide II).
OS   Carausius morosus (Indian stick insect), and
OS   Extatosoma tiaratum (Stick insect).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Phasmatodea; Heteronemiidae;
OC   Carausius.
OX   NCBI_TaxID=7022, 7024;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=87157103; PubMed=3828078;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structure of the hypertrehalosaemic factor II from the
RT   corpus cardiacum of the Indian stick insect, Carausius morosus,
RT   determined by fast atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN   [3]
RP   CARBOHYDRATE-LINKAGE SITE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=93129188; PubMed=1482345;
RA   Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT   "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT   a stick insect corpus cardiacum.";
RL   Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S07157; S07157.
DR   PIR; S09138; S09138.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Glycoprotein.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD      8      8       C-LINKED (MAN) (PROBABLE).
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1164 MW;  9B9036745771A9D1 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 KLVF 7
           :| |
Db       1 QLTF 4


RESULT 44
HTF_HELZE
ID   HTF_HELZE      STANDARD;      PRT;    10 AA.
AC   P16353;
DT   01-AUG-1990 (Rel. 15, Created)
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DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic hormone (HeZ-HRTH).
OS   Heliothis zea (Corn earworm) (Bollworm).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
OX   NCBI_TaxID=7113;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=88326324; PubMed=3415690;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA   Tseng C.M., Zhang Y.S., Hayes D.K.;
RT   "Isolation and primary structure of a neuropeptide hormone from
RT   Heliothis zea with hypertrehalosemic and adipokinetic activities.";
RL   Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A31571; A31571.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1096 MW;  8E70367865A5B9D1 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 KLVF 7
          :| |
Db      1 QLTF 4


RESULT 45
HTF_TABAT
ID   HTF_TABAT      STANDARD;      PRT;     10 AA.
AC   P14596;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE   (DCC II).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC   Tabanidae; Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; B33995; B33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1169 MW;  916036786771A9D1 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 KLVF 7
          :| |
Db      1 QLTF 4


RESULT 46
Q2OB_COMTE
ID   Q2OB_COMTE     STANDARD;      PRT;     10 AA.
AC   P80465;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS   Comamonas testosteroni (Pseudomonas testosteroni).
OC   Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
OX   NCBI_TaxID=285;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=63;
RX   MEDLINE=96035889; PubMed=7556204;
RA   Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT   "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT   dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT   quinoline and 3-methylquinoline degradation.";
RL   Eur. J. Biochem. 232:536-544(1995).
CC   -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)2-OXO-
CC       1,2-DIHYDROQUINOLINE.
CC   -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC       1(2H)-one + reduced acceptor.
CC   -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC   -!- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND
CC       (3-METHYL-)QUINOLINE.
CC   -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC       TWO GAMMA CHAINS (PROBABLE).
KW   Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1241 MW;  C2E2C25DD9CDC769 CRC64;

  Query Match             20.0%;  Score 11;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+04;
  Matches    3;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 KLVFFA 9
          |   ||
Db      2 KFPAFA 7


RESULT 47
BPP7_BOTIN
ID   BPP7_BOTIN     STANDARD;      PRT;     5 AA.
AC   P30425;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE   enzyme inhibitor).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8723;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
```

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RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC       ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC       BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC       IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR   PIR; G37196; G37196.
KW   Hypotensive agent; Venom.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   5 AA;  629 MW;  776DC37326B00000 CRC64;

  Query Match             18.2%;  Score 10;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 QK 4
          ||
Db      1 QK 2


RESULT 48
ACI_THUAL
ID   ACI_THUAL      STANDARD;      PRT;     8 AA.
AC   P18691;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-NOV-1990 (Rel. 16, Last annotation update)
DE   Angiotensin-converting enzyme inhibitor.
OS   Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8236;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Muscle;
RX   MEDLINE=88326322; PubMed=3415688;
RA   Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT   "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT   muscle.";
RL   Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR   PIR; A31570; A31570.
SQ   SEQUENCE   8 AA;  953 MW;  6AA863733051F1B7 CRC64;

  Query Match             18.2%;  Score 10;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQK 4
          | |
Db      3 HIK 5


RESULT 49
ALL1_CYDPO
ID   ALL1_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82152;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 1.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  934 MW;  C82879C45B51F775 CRC64;

  Query Match             18.2%;  Score 10;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HH 2
          |:
Db      3 HY 4


RESULT 50
LCK8_LEUMA
ID   LCK8_LEUMA     STANDARD;      PRT;     8 AA.
AC   P19990;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Last annotation update)
DE   Leucokinin VIII (L-VIII).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blaberoidea; Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Head;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Isolation, primary structure and synthesis of leucokinins VII and
RT   VIII: the final members of this new family of cephalomyotropic
RT   peptides isolated from head extracts of Leucophaea maderae.";
RL   Comp. Biochem. Physiol. 88C:31-34(1987).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR   PIR; JS0318; JS0318.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  902 MW;  736365AB59CAADD8 CRC64;

  Query Match             18.2%;  Score 10;  DB 1;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1e+05;
  Matches    1;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          |::
Db      4 FYS 6


Search completed: October 29, 2002, 09:37:57
Job time : 13 secs
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:32:02 ; Search time 24 Seconds
(without alignments)
72.081 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	21	38.2	9	10	P82440	P82440 nicotiana t
2	19	34.5	9	8	Q9GD36	Q9gd36 juncus effu
3	18	32.7	9	11	Q924N8	Q924n8 mus musculu
4	17	30.9	10	12	O39952	O39952 hepatitis g
5	17	30.9	10	12	Q9WLE4	Q9wle4 hepatitis g
6	16	29.1	5	13	P82070	P82070 litoria rub
7	16	29.1	5	13	P82071	P82071 litoria rub
8	16	29.1	8	4	Q15894	Q15894 homo sapien
9	16	29.1	8	10	Q40530	Q40530 nicotiana t
10	16	29.1	9	2	Q47556	Q47556 escherichia
11	16	29.1	9	4	Q9H4M8	Q9h4m8 homo sapien
12	15	27.3	8	2	Q9R5L7	Q9r517 clostridium
13	15	27.3	8	3	O13591	O13591 saccharomyc
14	15	27.3	8	4	Q15889	Q15889 homo sapien
15	15	27.3	9	2	O30790	O30790 erwinia amy
16	15	27.3	9	2	Q46179	Q46179 clostridium
17	15	27.3	9	6	Q9TT77	Q9tt77 bos taurus
18	15	27.3	9	12	O92766	O92766 canine dist
19	15	27.3	10	2	Q9R7J8	Q9r7j8 helicobacte
20	15	27.3	10	4	Q9UCS3	Q9ucs3 homo sapien
21	15	27.3	10	5	P82223	P82223 bombyx mori
22	15	27.3	10	5	P82224	P82224 bombyx mori
23	14	25.5	8	4	Q9UMH9	Q9umh9 homo sapien
24	14	25.5	9	4	Q9UC36	Q9uc36 homo sapien
25	14	25.5	9	8	Q94VG2	Q94vg2 varanus ind
26	14	25.5	10	10	P82937	P82937 hordeum vul
27	13	23.6	8	2	O09258	O09258 synechococc
28	13	23.6	8	2	Q9S6D5	Q9s6d5 escherichia
29	13	23.6	8	2	Q56759	Q56759 xanthobacte
30	13	23.6	8	4	Q9UDZ4	Q9udz4 homo sapien
31	13	23.6	8	5	O15899	O15899 babesia ovi
32	13	23.6	8	6	Q9GMH3	Q9gmh3 lagenorhync
33	13	23.6	8	6	Q28866	Q28866 megaptera n
34	13	23.6	8	6	O02831	O02831 oryctolagus
35	13	23.6	8	11	Q99NX9	Q99nx9 hydrochoeru
36	13	23.6	9	4	Q15891	Q15891 homo sapien
37	13	23.6	9	6	Q9GJV3	Q9gjv3 lagenorhync
38	13	23.6	9	6	Q9GJV2	Q9gjv2 lagenorhync
39	13	23.6	9	6	Q9GJV1	Q9gjv1 lagenorhync
40	13	23.6	9	8	Q9T688	Q9t688 gecko gecko
41	13	23.6	10	8	Q9T4P9	Q9t4p9 liolaemus d
42	13	23.6	10	8	Q9ZYV3	Q9zyv3 dipsosaurus
43	13	23.6	10	8	Q9ZYV0	Q9zyv0 petrosaurus
44	13	23.6	10	8	Q9ZYU7	Q9zyu7 sator angus
45	13	23.6	10	8	Q9ZYU4	Q9zyu4 sceloporus
46	13	23.6	10	8	Q9ZYU1	Q9zyu1 uma scopari
47	13	23.6	10	8	Q9ZYT8	Q9zyt8 urosaurus g
48	13	23.6	10	8	Q9ZYT5	Q9zyt5 uta stansbu
49	13	23.6	10	8	Q9ZYS9	Q9zys9 phymaturus
50	13	23.6	10	8	Q9TG98	Q9tg98 shinisaurus

ALIGNMENTS

RESULT 1
P82440
ID P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 42 KDA CELL WALL PROTEIN (FRAGMENT).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;

Query Match 38.2%; Score 21; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.6e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy      3 QKLVFFA 9
          :: ||||
Db      3 EESVFFA 9
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```
RESULT 2
Q9GD36
ID   Q9GD36      PRELIMINARY;      PRT;     9 AA.
AC   Q9GD36;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RIBOSOMAL PROTEIN S16 (FRAGMENT).
GN   RPS16.
OS   Juncus effusus.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; Juncus.
OX   NCBI_TaxID=13579;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LEAF;
RA   Asmussen C.B., Chase M.W.;
RT   "Coding and noncoding plastid DNA in palm systematics.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ404962; CAC17904.1; -.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1135 MW;  8DCCC9D2C046CB41 CRC64;

  Query Match             34.5%;  Score 19;  DB 8;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          ::|||
Db      4 QIVFF 8


RESULT 3
Q924N8
ID   Q924N8      PRELIMINARY;      PRT;     9 AA.
AC   Q924N8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   NIEMANN PICK TYPE C1 PROTEIN (FRAGMENT).
GN   NPC1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BLKS;
RA   Gevry N.Y., Lacroix D.A., Murphy B.D.;
RT   "Niemann-Pick C1 protein gene, partial cds and promotor region.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF184964; AAK83683.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  890 MW;  2C4E2DC761E1EDD8 CRC64;

  Query Match             32.7%;  Score 18;  DB 11;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HHQKL 5
          ||  |
Db      4 HHPAL 8


RESULT 4
O39952
ID   O39952      PRELIMINARY;      PRT;     10 AA.
AC   O39952;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   E1 PROTEIN (FRAGMENT).
OS   Hepatitis GB virus C.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC   GBV-C/HGV group.
OX   NCBI_TaxID=39839;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ED_INBURGH HAEMOPHILIAC;
RX   MEDLINE=97368412; PubMed=9225026;
RA   Smith D.B., Cuceanu N., Davidson F., Jarvis L.M., Mokili J.L.,
RA   Hamid S., Ludlam C.A., Simmonds P.;
RT   "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT   analysis of the 5' non-coding region.";
RL   J. Gen. Virol. 78:1533-1542(1997).
DR   EMBL; AF003170; AAC57981.1; -.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1152 MW;  CC88F0C9C7272732 CRC64;

  Query Match             30.9%;  Score 17;  DB 12;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 5.8e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          |:||
Db      5 LLFF 8


RESULT 5
Q9WLE4
ID   Q9WLE4      PRELIMINARY;      PRT;     10 AA.
AC   Q9WLE4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   POLYPROTEIN (FRAGMENT).
OS   Hepatitis G virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC   GBV-C/HGV group.
OX   NCBI_TaxID=45255;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SG3403;
RX   MEDLINE=99266893; PubMed=10335862;
RA   Wong S.B.J., Chan S.H., Ren E.C.;
RT   "Diversity of GB virus C/hepatitis G virus isolates in Singapore:
RT   predominance of group 2a and the Asian group 3 variant.";
RL   J. Med. Virol. 58:145-153(1999).
DR   EMBL; AF078063; AAC32369.1; -.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1152 MW;  CC88F0C9C7272732 CRC64;

  Query Match             30.9%;  Score 17;  DB 12;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 5.8e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          |:||
Db      5 LLFF 8


RESULT 6
P82070
ID   P82070      PRELIMINARY;      PRT;     5 AA.
AC   P82070;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 1.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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```
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  598 MW;  6DD9C9CAB2A00000 CRC64;

  Query Match             29.1%;  Score 16;  DB 13;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FFA 9
           |||
Db       3 FFA 5


RESULT 7
P82071
ID   P82071      PRELIMINARY;      PRT;     5 AA.
AC   P82071;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  626 MW;  6DD9C9CB10300000 CRC64;

  Query Match             29.1%;  Score 16;  DB 13;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FFA 9
           |||
Db       3 FFA 5


RESULT 8
Q15894
ID   Q15894      PRELIMINARY;      PRT;     8 AA.
AC   Q15894;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   (CLONE XP587B) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32074; AAA73884.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  952 MW;  EBC735B1E1F1B6D6 CRC64;

  Query Match             29.1%;  Score 16;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HH 2
           ||
Db       4 HH 5


RESULT 9
Q40530
ID   Q40530      PRELIMINARY;      PRT;     8 AA.
AC   Q40530;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   P20 N WITH A LEADER PEPTIDE.
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87089808; PubMed=3540612;
RA   Herman L.M.F., Montagu M.C.V., Depicker A.G.;
RT   "Isolation of tobacco DNA segments with plant promoter activity.";
RL   Mol. Cell. Biol. 6:4486-4492(1986).
DR   EMBL; M14685; AAA34090.1; -.
SQ   SEQUENCE   8 AA;  1109 MW;  E257205B19C9C9C6 CRC64;

  Query Match             29.1%;  Score 16;  DB 10;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       6 VFFAE 10
           :|| |
Db       1 MFFFE 5


RESULT 10
Q47556
ID   Q47556      PRELIMINARY;      PRT;     9 AA.
AC   Q47556;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ASPARTATE TRANSCARBAMOYLASE REGULATORY CHAIN (FRAGMENT).
GN   PYRI.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82275057; PubMed=7051000;
RA   Pauza C.D., Karels M.J., Navre M., Schachman H.K.;
RT   "Genes encoding Escherichia coli aspartate transcarbamoylase: The
RT   pyrB-pyrI operon.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
RN   [2]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE=83195078; PubMed=6302686;
RA   Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
RA   Wild J.R.;
RT   "Nucleotide sequence of the structural gene (pyrB) that encodes the
RT   catalytic polypeptide of aspartate transcarbamoylase of Escherichia
RT   coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
DR   EMBL; J01670; AAA24475.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1085 MW;  99EFD723344AA1F1 CRC64;

  Query Match             29.1%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HHQKL 5
          |  ||
Db      3 HDNKL 7


RESULT 11
Q9H4M8
ID   Q9H4M8      PRELIMINARY;      PRT;     9 AA.
AC   Q9H4M8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   PAR2 (FRAGMENT).
GN   NR1I2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RA   Pentecost B.T., Ling G.;
RT   "The human pregnane X receptor promoter complex provides
RT   transcriptional starts for a number of PXR related transcripts.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY007189; AAG23345.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1129 MW;  82F8E1F1B411B2D1 CRC64;

  Query Match             29.1%;  Score 16;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HH 2
          ||
Db      7 HH 8


RESULT 12
Q9R5L7
ID   Q9R5L7      PRELIMINARY;      PRT;     8 AA.
AC   Q9R5L7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   1,4-BETA-D-GLUCAN GLUCANOHYDROLASE (EC 3.2.1.4) (FRAGMENT).
OS   Clostridium thermocellum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1515;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92231850; PubMed=1567379;
RA   Romaniec M.P., Fauth U., Kobayashi T., Huskisson N.S., Barker P.J.,
RA   Demain A.L.;
RT   "Purification and characterization of a new endoglucanase from
RT   Clostridium thermocellum.";
RL   Biochem. J. 283:69-73(1992).
SQ   SEQUENCE   8 AA;  823 MW;  C2C1AB1DD9D1B775 CRC64;

  Query Match             27.3%;  Score 15;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      8 FAE 10
          |||
Db      4 FAE 6


RESULT 13
O13591
ID   O13591      PRELIMINARY;      PRT;     8 AA.
AC   O13591;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ORF YNL337W (FRAGMENT).
GN   YNL337W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Obermaier B., Piravandi E., Rinke M.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   MIPS;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z71612; CAA96271.2; -.
DR   SGD; S0005281; YNL337W.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1005 MW;  5CA441E449C9C720 CRC64;

  Query Match             27.3%;  Score 15;  DB 3;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          ::||
Db      1 ILFF 4


RESULT 14
Q15889
ID   Q15889      PRELIMINARY;      PRT;     8 AA.
AC   Q15889;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   (CLONE XP15H8B) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
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RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32070; AAA73879.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  865 MW;  0474472325A761E7 CRC64;

  Query Match             27.3%;  Score 15;  DB 4;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HHQKL 5
          |  ||
Db      2 HPSKL 6


RESULT 15
O30790
ID   O30790      PRELIMINARY;      PRT;     9 AA.
AC   O30790;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   STREPTOMYCIN RESISTANCE PROTEIN A (FRAGMENT).
GN   STRA.
OS   Erwinia amylovora.
OG   Plasmid pEa8.7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Erwinia.
OX   NCBI_TaxID=552;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CA3R;
RX   MEDLINE=98027397; PubMed=9361446;
RA   Palmer E.L., Teviotdale B.L., Jones A.L.;
RT   "A relative of the broad-host-range plasmid RSF1010 detected in
RT   Erwinia amylovora.";
RL   Appl. Environ. Microbiol. 63:4604-4607(1997).
DR   EMBL; AF017389; AAC45877.1; -.
KW   Plasmid.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1099 MW;  0140C9C05451B404 CRC64;

  Query Match             27.3%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 VFF 8
          :||
Db      6 IFF 8


RESULT 16
Q46179
ID   Q46179      PRELIMINARY;      PRT;     9 AA.
AC   Q46179;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHLORAMPHENICOL ACETYLTRANSFERASE.
GN   CATQ.
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CW 531;
RX   MEDLINE=91247774; PubMed=2039197;
RA   Bannam T.L., Rood J.I.;
RT   "The relationship between the Clostridium perfringens catQ gene
RT   product and chloramphenicol acetyltransferases from other bacteria.";
RL   Antimicrob. Agents Chemother. 35:471-476(1991).
DR   EMBL; M55620; AAA23214.1; -.
KW   Transferase.
SQ   SEQUENCE   9 AA;  1041 MW;  AFF4D72322CDD696 CRC64;

  Query Match             27.3%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 KLVF 7
          || |
Db      6 KLAF 9


RESULT 17
Q9TT77
ID   Q9TT77      PRELIMINARY;      PRT;     9 AA.
AC   Q9TT77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   WILM'S TUMOR PROTEIN 1 (FRAGMENT).
GN   WT1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21015404; PubMed=11130975;
RA   Brouillette J.A., Andrew J.R., Venta P.J.;
RT   "Estimate of nucleotide diversity in dogs with a pool-and-sequence
RT   method.";
RL   Mamm. Genome 11:1079-1086(2000).
DR   EMBL; AF202074; AAF20919.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1231 MW;  58DDF41416D1F403 CRC64;

  Query Match             27.3%;  Score 15;  DB 6;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQK 4
          ||:
Db      4 HQR 6


RESULT 18
O92766
ID   O92766      PRELIMINARY;      PRT;     9 AA.
AC   O92766;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   FUSION PROTEIN (FRAGMENT).
GN   F.
OS   canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DOG #5526/89;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026237; AAC09167.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1011 MW;  F281732760533441 CRC64;
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  Query Match             27.3%;  Score 15;  DB 12;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKL 5
          | |:
Db      2 HNKI 5


RESULT 19
Q9R7J8
ID   Q9R7J8      PRELIMINARY;      PRT;    10 AA.
AC   Q9R7J8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   VACUOLATING CYTOTOXIN (FRAGMENT).
GN   VACA.
OS   Helicobacter pylori (Campylobacter pylori).
OC   Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC   Helicobacter.
OX   NCBI_TaxID=210;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=KOBE 500;
RA   Shirasaka D.;
RT   "Helicobacter pylori vacA gene, strain Kobe 500, partial cds.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB017599; BAA33412.1; -.
FT   NON_TER       1      1
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1018 MW;  414390C76879CDD7 CRC64;

  Query Match             27.3%;  Score 15;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+04;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 KLVF 7
          || |
Db      2 KLAF 5


RESULT 20
Q9UCS3
ID   Q9UCS3      PRELIMINARY;      PRT;    10 AA.
AC   Q9UCS3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   TROPOMYOSIN-33 KDA CALCIUM BINDING PROTEIN FRAGMENT D.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92090441; PubMed=1836432;
RA   Crabos M., Yamakado T., Heizmann C.W., Cerletti N., Buhler F.R.,
RA   Erne P.;
RT   "The calcium binding protein tropomyosin in human platelets and
RT   cardiac tissue: elevation in hypertensive cardiac hypertrophy.";
RL   Eur. J. Clin. Investig. 21:472-478(1991).
SQ   SEQUENCE   10 AA;  1126 MW;  7A44FD3DC2DAFAEB CRC64;

  Query Match             27.3%;  Score 15;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      8 FAE 10
          |||
Db      1 FAE 3


RESULT 21
P82223
ID   P82223      PRELIMINARY;      PRT;    10 AA.
AC   P82223;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   UNKNOWN PROTEIN FROM 2D-PAGE (FRAGMENT).
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Bombycoidea; Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
RX   MEDLINE=21177481; PubMed=11280994;
RA   Zhong B.X.;
RT   "Protein database for several tissues derived from five instar of
RT   silkworm.";
RL   I Chuan Hsueh Pao 28:217-224(2001).
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1054 MW;  D0F722C325B1F1B2 CRC64;

  Query Match             27.3%;  Score 15;  DB 5;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+04;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKLV 6
          | |::
Db      5 HSKVL 9


RESULT 22
P82224
ID   P82224      PRELIMINARY;      PRT;    10 AA.
AC   P82224;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   UNKNOWN PROTEIN FROM 2D-PAGE (FRAGMENT).
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Bombycoidea; Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
RX   MEDLINE=21177481; PubMed=11280994;
RA   Zhong B.X.;
RT   "Protein database for several tissues derived from five instar of
RT   silkworm.";
RL   I Chuan Hsueh Pao 28:217-224(2001).
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1064 MW;  D77CBF25B1F1B2CD CRC64;

  Query Match             27.3%;  Score 15;  DB 5;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+04;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKLV 6
          | |::
Db      6 HSKVL 10


RESULT 23
Q9UMH9
ID   Q9UMH9      PRELIMINARY;      PRT;     8 AA.
AC   Q9UMH9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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DE   RHCE PROTEIN (FRAGMENT).
GN   RHCE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=97260406; PubMed=9106526;
RA   Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.;
RT   "Characterization of the recombination hot spot involved in the
RT   genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT   phenotype.";
RL   Am. J. Hum. Genet. 60:808-817(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=90349591; PubMed=1696722;
RA   Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
RA   Hermand P., Salmon C., Cartron J.-P., Colin Y.;
RT   "Molecular cloning and protein structure of a human blood group Rh
RT   polypeptide.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
DR   EMBL; Z97030; CAB09726.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  1049 MW;  C007244691FB5AB1 CRC64;

  Query Match             25.5%;  Score 14;  DB 4;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HHQKL 5
          :|  |
Db      3 YHMNL 7


RESULT 24
Q9UC36
ID   Q9UC36      PRELIMINARY;      PRT;     9 AA.
AC   Q9UC36;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   28 KDA HEAT SHOCK PROTEIN HOMOLOG FRAGMENT 1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92218434; PubMed=1560006;
RA   Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT   "Copurification of small heat shock protein with alpha B crystallin
RT   from human skeletal muscle.";
RL   J. Biol. Chem. 267:7718-7725(1992).
SQ   SEQUENCE   9 AA;  1220 MW;  26933415B1F77B43 CRC64;

  Query Match             25.5%;  Score 14;  DB 4;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 HQKL 5
          | :|
Db      5 HSRL 8


RESULT 25
Q94VG2
ID   Q94VG2      PRELIMINARY;      PRT;     9 AA.
AC   Q94VG2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Varanus indicus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX   NCBI_TaxID=62043;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ast J.C.;
RT   "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL   Cladistics 17:0-0(2001).
DR   EMBL; AF407505; AAL10069.1; -.
KW   Mitochondrion.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1258 MW;  881259C727336411 CRC64;

  Query Match             25.5%;  Score 14;  DB 8;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 LVFF 8
          |:|:
Db      5 LLFY 8


RESULT 26
P82937
ID   P82937      PRELIMINARY;      PRT;     10 AA.
AC   P82937;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN ENDOSPERM PROTEIN B (FRAGMENT).
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. BOMI; TISSUE=STARCHY ENDOSPERM;
RX   MEDLINE=21088911; PubMed=11271488;
RA   Kristoffersen H.E., Flengsrud R.;
RT   "Separation and characterization of basic barley seed proteins.";
RL   Electrophoresis 21:3693-3700(2000).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 KDA.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1297 MW;  8248A50B11FB5EBA CRC64;

  Query Match             25.5%;  Score 14;  DB 10;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 2.2e+04;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQK 4
          :|::
Db      5 YHER 8


RESULT 27
O09258
ID   O09258      PRELIMINARY;      PRT;     8 AA.
AC   O09258;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   NIFH (FRAGMENT).
GN   NIFH.
OS   Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801).
OC   Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
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OX   NCBI_TaxID=41431;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RF-1;
RX   MEDLINE=99231861; PubMed=10217509;
RA   Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT   "Organization and expression of nitrogen-fixation genes in the aerobic
RT   nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RT   RF-1.";
RL   Microbiology 145:743-753(1999).
DR   EMBL; AF001780; AAC33369.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  985 MW;  F16B59CDD046C406 CRC64;

  Query Match             23.6%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   16.7%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 QKLVFF 8
          ::: |:
Db      2 RQIAFY 7


RESULT 28
Q9S6D5
ID   Q9S6D5      PRELIMINARY;      PRT;     8 AA.
AC   Q9S6D5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   PUTATIVE IS30 TRANSPOSASE (FRAGMENT).
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A295B;
RX   MEDLINE=99194747; PubMed=10094716;
RA   Rahn A., Drummelsmith J., Whitfield C.;
RT   "Conserved organization in the cps gene clusters for expression of
RT   Escherichia coli group 1 K antigens: relationship to the colanic acid
RT   biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
RL   J. Bacteriol. 181:2307-2313(1999).
DR   EMBL; AF118251; AAD30008.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  1011 MW;  F21DC1A9D1B41406 CRC64;

  Query Match             23.6%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      7 FFAE 10
          | ||
Db      5 FTAE 8


RESULT 29
Q56759
ID   Q56759      PRELIMINARY;      PRT;     8 AA.
AC   Q56759;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HALOACID DEHALOGENASE (FRAGMENT).
GN   DHLB.
OS   Xanthobacter autotrophicus.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Hyphomicrobium group; Xanthobacter.
OX   NCBI_TaxID=280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GJ10, AND CV. M50;
RX   MEDLINE=95173113; PubMed=7868610;
RA   Van der Ploeg J., Willemsen M., van Hall G., Janssen D.B.;
RT   "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
RT   activation and mobilization of the haloacetate dehalogenase gene by
RT   insertion element IS1247.";
RL   J. Bacteriol. 177:1348-1356(1995).
DR   EMBL; X84038; CAA58857.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  922 MW;  F3A9D2D2CDD33056 CRC64;

  Query Match             23.6%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 KLVFF 8
          | | |
Db      3 KAVVF 7


RESULT 30
Q9UDZ4
ID   Q9UDZ4      PRELIMINARY;      PRT;     8 AA.
AC   Q9UDZ4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHD PROTEIN (FRAGMENT).
GN   RHD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=97260406; PubMed=9106526;
RA   Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.;
RT   "Characterization of the recombination hot spot involved in the
RT   genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT   phenotype.";
RL   Am. J. Hum. Genet. 60:808-817(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=93066356; PubMed=1438298;
RA   Le Van Kim C., Mouro I., Cherif-Zahar B., Raynal V., Cherrier C.,
RA   Cartron J.P., Colin Y.;
RT   "Molecular cloning and primary structure of the human blood group Rh
RT   polypeptide.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
DR   EMBL; Z97031; CAB09727.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  1042 MW;  D296944691FB5AB1 CRC64;

  Query Match             23.6%;  Score 13;  DB 4;  Length 8;
  Best Local Similarity   16.7%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HHQKLV 6
          :|  ::
Db      3 YHMNMM 8


RESULT 31
O15899
ID   O15899      PRELIMINARY;      PRT;     8 AA.
AC   O15899;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   12D3 ANTIGEN (FRAGMENT).
GN   BO12D3.
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OS   Babesia ovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5869;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ANKARA;
RA   Silins G.U., Blakeley R.L., Riddles P.W.;
RT   "Characterization of the transcriptional control region of the 12D3
RT   antigen gene from the sporozoan Babesia bovis.";
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U44919; AAB66365.1; -.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  992 MW;  F0C7273411B2C726 CRC64;

  Query Match             23.6%;  Score 13;  DB 5;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KLVF 7
           :|:|
Db       5 RLLF 8


RESULT 32
Q9GMH3
ID   Q9GMH3      PRELIMINARY;      PRT;     8 AA.
AC   Q9GMH3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ACTIN (FRAGMENT).
OS   Lagenorhynchus obscurus (dusky dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Lagenorhynchus.
OX   NCBI_TaxID=27611;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hare M.P., Cipriano F., Palumbi S.R.;
RT   "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT   Speciation, Systematics and Conservation.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF140833; AAF98686.1; -.
FT   NON_TER       1       1
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  962 MW;  5BD1F417740862C0 CRC64;

  Query Match             23.6%;  Score 13;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQ 3
           ||
Db       7 HQ 8


RESULT 33
Q28866
ID   Q28866      PRELIMINARY;      PRT;     8 AA.
AC   Q28866;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   ACTIN PROTEIN (FRAGMENT).
GN   ACTIN.
OS   Megaptera novaeangliae (Humpback whale).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC   Balaenopteridae; Megaptera.
OX   NCBI_TaxID=9773;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94285813; PubMed=7912407;
RA   Palumbi S.R., Baker C.S.;
RT   "Contrasting population structure from nuclear intron sequences and
RT   mtDNA of humpback whales.";
RL   Mol. Biol. Evol. 11:426-435(1994).
DR   EMBL; S73467; AAD14118.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  906 MW;  69C866D1F4177408 CRC64;

  Query Match             23.6%;  Score 13;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQ 3
           ||
Db       5 HQ 6


RESULT 34
O02831
ID   O02831      PRELIMINARY;      PRT;     8 AA.
AC   O02831;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96377339; PubMed=8783186;
RA   Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA   Vuorio E.;
RT   "Evidence for insufficient chondrocytic differentiation during repair
RT   of full-thickness defects of articular cartilage.";
RL   Matrix Biol. 15:39-47(1996).
DR   EMBL; S83371; AAD14433.1; -.
KW   Collagen.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  1028 MW;  B859C7272EA77371 CRC64;

  Query Match             23.6%;  Score 13;  DB 6;  Length 8;
  Best Local Similarity   42.9%;  Pred. No. 5.6e+05;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 HHQKLVF 7
           |   |:|
Db       1 HWPCLLF 7


RESULT 35
Q99NX9
ID   Q99NX9      PRELIMINARY;      PRT;     8 AA.
AC   Q99NX9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AMYLOID BETA PROTEIN (FRAGMENT).
GN   APP.
OS   Hydrochoerus hydrochaeris (Capybara) (Carpincho).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
OC   Hydrochaeris.
OX   NCBI_TaxID=10149;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082082; PubMed=11214319;
RA   Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA   O'Brien S.J.;
RT   "Molecular phylogenetics and the origins of placental mammals.";
RL   Nature 409:614-618(2001).
DR   EMBL; AY011342; AAG47377.1; -.
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FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1071 MW;  1356D686DB19C9C3 CRC64;

  Query Match           23.6%;  Score 13;  DB 11;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      7 FFAE 10
          || :
Db      2 FFEQ 5


RESULT 36
Q15891
ID   Q15891      PRELIMINARY;      PRT;     9 AA.
AC   Q15891;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   (CLONE XP2E8B) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32131; AAA73881.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1030 MW;  E56635A1A33686D1 CRC64;

  Query Match           23.6%;  Score 13;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQ 3
          ||
Db      2 HQ 3


RESULT 37
Q9GJV3
ID   Q9GJV3      PRELIMINARY;      PRT;     9 AA.
AC   Q9GJV3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ACTIN (FRAGMENT).
OS   Lagenorhynchus obscurus (dusky dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Lagenorhynchus.
OX   NCBI_TaxID=27611;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hare M.P., Cipriano F., Palumbi S.R.;
RT   "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT   Speciation, Systematics and Conservation.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF140834; AAF98687.1; -.
DR   EMBL; AF140832; AAF98685.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1049 MW;  1D0EF417740862C0 CRC64;

  Query Match           23.6%;  Score 13;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQ 3
          ||
Db      8 HQ 9


RESULT 38
Q9GJV2
ID   Q9GJV2      PRELIMINARY;      PRT;     9 AA.
AC   Q9GJV2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ACTIN (FRAGMENT).
OS   Lagenorhynchus obliquidens (Pacific white-sided dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Lagenorhynchus.
OX   NCBI_TaxID=90247;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hare M.P., Cipriano F., Palumbi S.R.;
RT   "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT   Speciation, Systematics and Conservation.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF140831; AAF98684.1; -.
DR   EMBL; AF140826; AAF98679.1; -.
DR   EMBL; AF140827; AAF98680.1; -.
DR   EMBL; AF140828; AAF98681.1; -.
DR   EMBL; AF140829; AAF98682.1; -.
DR   EMBL; AF140830; AAF98683.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1049 MW;  1D0EF417740862C0 CRC64;

  Query Match           23.6%;  Score 13;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 HQ 3
          ||
Db      8 HQ 9


RESULT 39
Q9GJV1
ID   Q9GJV1      PRELIMINARY;      PRT;     9 AA.
AC   Q9GJV1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ACTIN (FRAGMENT).
OS   Lagenorhynchus acutus (Atlantic white-sided dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Lagenorhynchus.
OX   NCBI_TaxID=90246;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hare M.P., Cipriano F., Palumbi S.R.;
RT   "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT   Speciation, Systematics and Conservation.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF140825; AAF98678.1; -.
DR   EMBL; AF140822; AAF98675.1; -.
DR   EMBL; AF140823; AAF98676.1; -.
DR   EMBL; AF140824; AAF98677.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1049 MW;  1D0EF417740862C0 CRC64;
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  Query Match             23.6%;  Score 13;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 HQ 3
           ||
Db       8 HQ 9


RESULT 40
Q9T688
ID   Q9T688      PRELIMINARY;      PRT;     9 AA.
AC   Q9T688;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Gecko gecko (Tokay gecko).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
OX   NCBI_TaxID=36310;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99343618; PubMed=10413626;
RA   Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
RT   "Vicariant patterns of fragmentation among gekkonid lizards of the
RT   genus teratoscincus produced by the indian collision: A molecular
RT   phylogenetic perspective and an area cladogram for central asia.";
RL   Mol. Phylogenet. Evol. 12:320-332(1999).
DR   EMBL; AF114249; AAD51600.1; -.
KW   Mitochondrion.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1188 MW;  428CB9C9D36411A7 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 5.6e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FFA 9
           ||:
Db       6 FFS 8


RESULT 41
Q9T4P9
ID   Q9T4P9      PRELIMINARY;      PRT;     10 AA.
AC   Q9T4P9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Liolaemus darwinii.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX   NCBI_TaxID=109408;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SDSU3477, AND SDSU3472;
RA   Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT   "Phylogenetic Relationships in the Iguanid Lizard Genus Liolaemus:
RT   Multiple Origins of Viviparous Reproduction and a Phylogenetic
RT   Evaluation of Andean Vicariance.";
RL   Biol. J. Linn. Soc. Lond. 0:0-0(2000).
DR   EMBL; AF099274; AAF18928.1; -.
DR   EMBL; AF099272; AAF18922.1; -.
KW   Mitochondrion.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1288 MW;  1A3580C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FFA 9
           ||:
Db       7 FFS 9


RESULT 42
Q9ZYV3
ID   Q9ZYV3      PRELIMINARY;      PRT;     10 AA.
AC   Q9ZYV3;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Dipsosaurus dorsalis.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Dipsosaurus.
OX   NCBI_TaxID=51217;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049857; AAD02514.1; -.
KW   Mitochondrion.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1275 MW;  1A3580C9D36411A0 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 FFA 9
           ||:
Db       7 FFS 9


RESULT 43
Q9ZYV0
ID   Q9ZYV0      PRELIMINARY;      PRT;     10 AA.
AC   Q9ZYV0;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Petrosaurus thalassinus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC   Petrosaurus.
OX   NCBI_TaxID=81826;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049858; AAD02517.1; -.
KW   Mitochondrion.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1288 MW;  1A3580C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
```

```
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 44
Q9ZYU7
ID   Q9ZYU7      PRELIMINARY;      PRT;    10 AA.
AC   Q9ZYU7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Sator angustus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Sator.
OX   NCBI_TaxID=43619;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049859; AAD02520.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1288 MW;  1A3580C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 45
Q9ZYU4
ID   Q9ZYU4      PRELIMINARY;      PRT;    10 AA.
AC   Q9ZYU4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Sceloporus graciosus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC   Sceloporus.
OX   NCBI_TaxID=43625;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049860; AAD02523.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1365 MW;  129780C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 46
Q9ZYU1
ID   Q9ZYU1      PRELIMINARY;      PRT;    10 AA.
AC   Q9ZYU1;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Uma scoparia.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uma.
OX   NCBI_TaxID=81829;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049861; AAD02526.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1288 MW;  1A3580C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 47
Q9ZYT8
ID   Q9ZYT8      PRELIMINARY;      PRT;    10 AA.
AC   Q9ZYT8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Urosaurus graciosus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC   Urosaurus.
OX   NCBI_TaxID=43647;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049862; AAD02529.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1288 MW;  1A3580C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
```

```
Db      7 FFS 9


RESULT 48
Q9ZYT5
ID   Q9ZYT5      PRELIMINARY;      PRT;    10 AA.
AC   Q9ZYT5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Uta stansburiana.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX   NCBI_TaxID=43653;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049863; AAD02532.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1288 MW;  1A3580C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 49
Q9ZYS9
ID   Q9ZYS9      PRELIMINARY;      PRT;    10 AA.
AC   Q9ZYS9;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Phymaturus somuncurensis.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Phymaturus.
OX   NCBI_TaxID=81831;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049865; AAD02538.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1288 MW;  1A3580C9D3640440 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


RESULT 50
Q9TG98
ID   Q9TG98      PRELIMINARY;      PRT;    10 AA.
AC   Q9TG98;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN   COI.
OS   Shinisaurus crocodilurus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Shinisauridae;
OC   Shinisaurus.
OX   NCBI_TaxID=52224;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99343613; PubMed=10413621;
RA   Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
RA   Papenfuss T.J.;
RT   "Molecular phylogenetics, tRNA evolution, and historical biogeography
RT   in anguid lizards and related taxonomic families.";
RL   Mol. Phylogenet. Evol. 12:250-272(1999).
DR   EMBL; AF085604; AAD51502.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1290 MW;  1CEE80C9D36411A0 CRC64;

  Query Match             23.6%;  Score 13;  DB 8;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 FFA 9
          ||:
Db      7 FFS 9


Search completed: October 29, 2002, 09:38:29
Job time : 26 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:26 ; Search time 31 Seconds
(without alignments)
35.830 Million cell updates/sec

Title: US-09-724-842A-27
Perfect score: 55
Sequence: 1 HHQKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	10	22	AAB46225	Human APP derived
2	55	100.0	15	20	AAW89358	Beta-amyloid pepti
3	55	100.0	17	15	AAR54703	Beta-amyloid fragm
4	55	100.0	17	22	AAB91774	Amyloid beta-prote
5	55	100.0	17	22	AAB91807	Amyloid beta-prote
6	55	100.0	17	22	AAB48346	Beta-amyloid antig
7	55	100.0	18	21	AAB10963	Beta-amyloid precu
8	55	100.0	19	18	AAW18882	AEDANS-beta-amyloi
9	55	100.0	19	18	AAW18881	Trp-Beta-amyloid p
10	55	100.0	19	22	AAB46201	Human APP A-beta 1
11	55	100.0	19	22	AAB49097	Human amyloid beta
12	55	100.0	21	20	AAY30941	Human secretase SE
13	55	100.0	24	15	AAR52569	Alzheimer's diseas
14	55	100.0	26	19	AAW47229	Beta-amyloid pepti
15	55	100.0	26	20	AAY33408	Human amyloidogeni
16	55	100.0	27	20	AAY33409	Human amyloidogeni
17	55	100.0	28	8	AAP70594	Sequence of Alzhei
18	55	100.0	28	10	AAP90381	Synthetic A4 amylo
19	55	100.0	28	15	AAR54702	Beta-amyloid fragm
20	55	100.0	28	15	AAR60368	Beta-amyloid (1-28
21	55	100.0	28	16	AAR64170	A4-O(1-28) a parti
22	55	100.0	28	16	AAR64171	A4-P(1-28) a parti
23	55	100.0	28	16	AAR64172	A4-B(1-28) a parti
24	55	100.0	28	16	AAR64164	Generic beta amylo
25	55	100.0	28	17	AAW01413	Beta/A4-amyloid pe
26	55	100.0	28	20	AAY39805	Beta-amyloid prote
27	55	100.0	28	20	AAW81467	Synthetic amyloid
28	55	100.0	28	22	AAB91783	Amyloid beta-prote
29	55	100.0	28	22	AAB91789	Amyloid beta-prote
30	55	100.0	28	22	AAB91800	Amyloid beta-prote
31	55	100.0	28	22	AAB91816	Amyloid beta-prote
32	55	100.0	28	22	AAB91827	Amyloid beta-prote
33	55	100.0	28	22	AAB49396	Human amyloid pept
34	55	100.0	28	22	AAB35590	Human clone B(1-28
35	55	100.0	28	22	AAB35591	Human clone D1N B(
36	55	100.0	28	22	AAB35592	Human clone E3Q B(
37	55	100.0	28	22	AAB35593	Human clone R5Q B(
38	55	100.0	28	22	AAB35594	Human clone H6Q B(
39	55	100.0	28	22	AAB35595	Human clone D7Q B(
40	55	100.0	28	22	AAB35596	Human clone E11Q B
41	55	100.0	28	22	AAB36201	Human clone D23Q B
42	55	100.0	28	22	AAB36202	Human clone K28Q B
43	55	100.0	30	20	AAW81468	Synthetic amyloid
44	55	100.0	32	22	AAB84430	Partial sequence o
45	55	100.0	33	20	AAW81469	Synthetic amyloid
46	55	100.0	35	19	AAW47228	Beta-amyloid pepti
47	55	100.0	35	20	AAW89357	Beta-amyloid pepti
48	55	100.0	35	20	AAW89359	Beta-amyloid pepti
49	55	100.0	35	20	AAW89361	Beta-amyloid pepti
50	55	100.0	36	20	AAW81471	Synthetic amyloid

ALIGNMENTS

RESULT 1
AAB46225
ID AAB46225 standard; peptide; 10 AA.
XX
AC AAB46225;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #21.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.

XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 1 HHQKLVFFAE 10

RESULT 2
AAW89358
ID AAW89358 standard; peptide; 15 AA.
XX
AC AAW89358;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-11-25.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Claim 6; Column 81-82; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 55; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 3 HHQKLVFFAE 12

RESULT 3
AAR54703
ID AAR54703 standard; peptide; 17 AA.
XX
AC AAR54703;
XX
DT 15-DEC-1994 (first entry)
XX
DE Beta-amyloid fragment (12-28).
XX
KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9409364-A.
XX
PD 28-APR-1994.
XX
PF 13-OCT-1993; 93WO-US09772.
XX
PR 13-OCT-1992; 92US-0959251.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Strittmatter WJ;
XX
DR WPI; 1994-151484/18.
XX
PT Immobilised beta-amyloid protein or fragments - used in assays
PT for obtaining prods for use in the diagnosis and treatment of
PT disorders such as Alzheimer's disease.
XX
PS Claim 5; Page 28; 49pp; English.
XX
CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp.
CC the peptides given in AAR54702-03) immobilised on a solid support can be
CC used to detect cpds. which bind to BAP. Binding of proteins in
CC human cerebrospinal fluid proteins were shown to bind to beta-
CC amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28)
CC was used as control.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 55; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10

```
                 ||||||||||
Db       2 HHQKLVFFAE 11

RESULT 4
AAB91774
ID   AAB91774 standard; Peptide; 17 AA.
XX
AC   AAB91774;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Amyloid beta-protein fragment peptide SEQ ID NO:950.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 504; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   17 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       2 HHQKLVFFAE 11

RESULT 5
AAB91807
ID   AAB91807 standard; Peptide; 17 AA.
XX
AC   AAB91807;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Amyloid beta-protein fragment peptide SEQ ID NO:983.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 516; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   17 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       2 HHQKLVFFAE 11

RESULT 6
AAB48346
ID   AAB48346 standard; peptide; 17 AA.
XX
AC   AAB48346;
XX
```

DT 20-APR-2001 (first entry)
XX
DE Beta-amyloid antigenic peptide (Abeta10-25).
XX
KW Beta-amyloid; nootropic; neuroprotective; vaccine; antibody; brain;
KW amyloid plaque; Alzheimer's disease; antigen.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 17
FT /note= "C-terminal amide"
XX
PN WO200077178-A1.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16551.
XX
PR 16-JUN-1999; 99US-0139408.
XX
PA (BOST-) BOSTON BIOMEDICAL RES INST.
XX
PI Raso V;
XX
DR WPI; 2001-112220/12.
XX
PT New antibodies which catalyze hydrolysis of beta-amyloid at a
PT predetermined amide linkage, useful for e.g. sequestering or reducing
PT free beta-amyloid in the bloodstream and brain and preventing formation
PT of amyloid plaques -
XX
PS Example 1; Fig 3; 82pp; English.
XX
CC The invention relates to an antibody which catalyzes the hydrolysis of
CC beta-amyloid at a predetermined amide linkage. The antibodies are useful
CC for sequestering free beta-amyloid in the bloodstream of an animal,
CC reducing beta-amyloid levels in the brain, preventing formation of
CC amyloid plaques, and disaggregating amyloid plaques present in the brain,
CC thus may be used in treating patients diagnosed with or at risk for
CC Alzheimer's disease. The present sequence represents a beta-amyloid
CC antigenic peptide made from the central region of beta-amyloid. The
CC antigenic peptides were designed to be tested for suitability to
CC antibody-mediated therapy.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 55; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 5 HHQKLVFFAE 14

RESULT 7
AAB10963
ID AAB10963 standard; protein; 18 AA.
XX
AC AAB10963;
XX
DT 07-FEB-2001 (first entry)
XX
DE Beta-amyloid precursor protein peptide fragment.
XX
KW APP; amyloid precursor protein; human; alpha-secretase; ADAM 10;
KW disintegrin-metalloprotease; protease; nootropic; neuroprotective;
KW gene therapy; Alzheimer's disease.
XX
OS Unidentified.
XX
PN DE19910108-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-1999; 99DE-1010108.
XX
PR 08-MAR-1999; 99DE-1010108.
XX
PA (FAHR/) FAHRENHOLZ F.
XX
PI Fahrenholz F, Postina R;
XX
DR WPI; 2000-588391/56.
XX
PT Recombinant cells, for identifying alpha-secretase active agents and
PT identifying risk factors associated with Alzheimer's disease, comprise
PT amyloid precursor protein and alpha-secretase -
XX
PS Example 13; Page 12; 24pp; German.
XX
CC This invention describes a novel recombinant cell comprising recombinant
CC nucleic acids encoding a region of human amyloid precursor protein
CC containing an alpha-secretase cleavage site and a protease or a
CC heterologous RNA coding for a substrate protein and a protease. The
CC invention also describes a recombinant cell, characterized in that it
CC contains recombinant nucleic acids comprising either: (a) a gene for a
CC substrate protein (SP), which comprises a sequence region of 18 amino
CC acids of the human amyloid precursor protein (APP) or a homologous
CC protein, where the sequence region contains the alpha-secretase cleavage
CC site at a reference of 6 residues at the N-terminal and 12 residues at
CC the C-terminal; and (b) a gene for a protease protein (PP), that either
CC comprises a proteolytically active necessary sequence region or a
CC sequence region of the disintegrin metalloprotease ADAM 10 from a cow
CC (Bos taurus), from a human or other mammal or a mutant of this, which
CC shows the same enzymatic properties, where the genes are under the
CC control of heterologous promoters; or a heterologous RNA coding for a SP
CC and a PP. The products of the invention have nootropic and
CC neuroprotective activity and can be used for gene therapy. The protease
CC proteins of the invention are useful for proteolytic cleavage of
CC substrate proteins, especially human amyloid precursor protein. Dominant
CC negative forms of bovine, human or other mammalian
CC disintegrin-metalloprotease ADAM 10 proteins and their coding sequences
CC are useful for suppressing the alpha-secretase activity of a cell.
CC Nucleic acid sequences encoding the proteases are useful for
CC constructing vectors for gene therapy. The proteins and recombinant cells
CC are useful for identifying secretases and pharmaceutical agents and to
CC identify risk factors associated with Alzheimer's disease.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 55; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 3 HHQKLVFFAE 12

RESULT 8
AAW18882
ID AAW18882 standard; peptide; 19 AA.
XX
AC AAW18882;
XX
DT 08-DEC-1997 (first entry)
XX
DE AEDANS-beta-amyloid peptide fragment (9-25).
XX
KW beta-amyloid peptide; membrane protein; amyloid precursor protein;
KW fibril assembly; in vitro; detection; fluorescence; amyloidosis disorder;
KW Alzheimer's disease; multiple myeloma; rheumatoid arthritis; diabetes;
KW prion disorder.
XX

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "AEDANS-Ac-Cys"
FT   Modified-site   19
FT                   /note= "Gly-CONH2"
XX
PN   WO9707402-A1.
XX
PD   27-FEB-1997.
XX
PF   16-AUG-1996;    96WO-CA00555.
XX
PR   17-AUG-1995;    95US-0515615.
XX
PA   (ONTA-) ONTARIO CANCER INST.
XX
PI   Chakrabartty A;
XX
DR   WPI; 1997-165446/15.
XX
PT   In vitro fluorescence monitoring of protein fibril assembly - esp.
PT   useful for monitoring fibril assembly processes associated with
PT   amyloidosis disorders, esp. Alzheimer's disease
XX
PS   Claim 26; Page 25; 40pp; English.
XX
CC   Beta-amyloid protein fibril assembly can be monitored using a new method
CC   for in vitro monitoring of peptide/protein fibril assembly using
CC   fluorescent energy transfer between closely juxtaposed donor and
CC   acceptor fluorophores. Two forms of beta-amyloid (9-25) were synthesised,
CC   one had a Trp residue attached to the N-terminus of the peptide
CC   (AAW18881), and the other (AAW18882) had a cysteine residue attached to
CC   the N-terminus, and an AEDANS group chemically linked to the sulfhydryl
CC   side chain of the cysteine. When both forms of beta-amyloid are mixed
CC   together, fibrils will assemble and in the fibril state the Trp and
CC   AEDANS groups will be closer in space than in the non-fibril state.
CC   Fluorescence energy transfer between Trp and AEDANS increases when the
CC   two fluorphores are close in space (i.e. efficiency of energy transfer
CC   will increase as the fibrils form) and the fluorescence can be measured.
CC   Fibril assembly processes associated with various amyloidosis disorders
CC   can be monitored by the method, especially Alzheimer's disease (claimed),
CC   multiple myeloma, rheumatoid arthritis, diabetes and prion disorders.
XX
SQ   Sequence   19 AA;

  Query Match             100.0%;  Score 55;  DB 18;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       7 HHQKLVFFAE 16


RESULT 9
AAW18881
ID   AAW18881 standard; peptide; 19 AA.
XX
AC   AAW18881;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Trp-Beta-amyloid peptide fragment (9-25).
XX
KW   beta-amyloid peptide; membrane protein; amyloid precursor protein;
KW   fibril assembly; in vitro; detection; fluorescence; amyloidosis disorder;
KW   Alzheimer's disease; multiple myeloma; rheumatoid arthritis; diabetes;
KW   prion disorder.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Acetyl-Trp"
FT   Modified-site   19
FT                   /note= "Gly-CONH2"
XX
PN   WO9707402-A1.
XX
PD   27-FEB-1997.
XX
PF   16-AUG-1996;    96WO-CA00555.
XX
PR   17-AUG-1995;    95US-0515615.
XX
PA   (ONTA-) ONTARIO CANCER INST.
XX
PI   Chakrabartty A;
XX
DR   WPI; 1997-165446/15.
XX
PT   In vitro fluorescence monitoring of protein fibril assembly - esp.
PT   useful for monitoring fibril assembly processes associated with
PT   amyloidosis disorders, esp. Alzheimer's disease
XX
PS   Claim 36; Page 25; 40pp; English.
XX
CC   Beta-amyloid protein fibril assembly can be monitored using a new method
CC   for in vitro monitoring of peptide/protein fibril assembly using
CC   fluorescent energy transfer between closely juxtaposed donor and
CC   acceptor fluorophores. Two forms of beta-amyloid (9-25) were synthesised,
CC   one had a Trp residue attached to the N-terminus of the peptide
CC   (AAW18881), and the other (AAW18882) had a cysteine residue attached to
CC   the N-terminus, and an AEDANS group chemically linked to the sulfhydryl
CC   side chain of the cysteine. When both forms of beta-amyloid are mixed
CC   together, fibrils will assemble and in the fibril state the Trp and
CC   AEDANS groups will be closer in space than in the non-fibril state.
CC   Fluorescence energy transfer between Trp and AEDANS increases when the
CC   two fluorphores are close in space (i.e. efficiency of energy transfer
CC   will increase as the fibrils form) and the fluorescence can be measured.
CC   Fibril assembly processes associated with various amyloidosis disorders
CC   can be monitored by the method, especially Alzheimer's disease (claimed),
CC   multiple myeloma, rheumatoid arthritis, diabetes and prion disorders.
XX
SQ   Sequence   19 AA;

  Query Match             100.0%;  Score 55;  DB 18;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       7 HHQKLVFFAE 16


RESULT 10
AAB46201
ID   AAB46201 standard; peptide; 19 AA.
XX
AC   AAB46201;
XX
DT   04-APR-2001  (first entry)
XX
DE   Human APP A-beta 13-28 peptide.
XX
KW   Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW   Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW   amyloid precursor protein; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200072880-A2.
XX
PD   07-DEC-2000.
```

XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
PS Disclosure; Page 61; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 55; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 1 HHQKLVFFAE 10

RESULT 11
AAB49097
ID AAB49097 standard; peptide; 19 AA.
XX
AC AAB49097;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human amyloid beta peptide (residues 13-28), SEQ ID NO:33.
XX
KW Amyloid disease; amyloid fibril deposition; amyloid plaque;
KW immunogenic; antibody; vaccine; Alzheimer's disease;
KW type 2 diabetes; reactive system amyloidosis;
KW systemic senile amyloidosis; familial amyloid cardiomyopathy;
KW transmissible spongiform encephalopathy; Creutzfeld-Jakob disease; Kuru;
KW haemodialysis-asssociated beta-2-microglobulin deposition;
KW amyloid beta peptide.
XX
OS Homo sapiens.
XX
PN WO200072876-A2.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15239.
XX
PR 01-JUN-1999; 99US-0137010.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB;
XX
DR WPI; 2001-070921/08.
XX
PT Pharmaceutical composition comprising immunogen against amyloid
PT component such as fibril peptide or protein, or antibody against
PT amyloid component useful for treating amyloid diseases or amyloidoses -
XX
PS Example IV; Page 74; 140pp; English.
XX
CC The invention relates to a novel pharmaceutical composition for
CC preventing or treating a disease characterised by amyloid fibril
CC deposits (amyloid plaques) in a patient. The pharmaceutical composition
CC comprises an agent that will induce an immune response against an amyloid
CC component, or an antibody or antibody fragment that binds to an amyloid
CC component. The invention also relates to a method for determining
CC the prognosis of a patient undergoing treatment for an amyloid disorder
CC which involves measuring a patient serum amount of immunoreactivity
CC against a selected amyloid component. A patient serum immunoreactivity
CC of at least four times a base line serum immunoreactivity control level
CC indicates a prognosis of improved status with respect to the disorder.
CC The pharmaceutical compositions of the invention are useful for treating
CC a wide variety of disorders characterised by amyloid fibril deposition in
CC a patient. Such disorders include Alzheimer's disease characterised by
CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by
CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
CC amyloidosis associated with systemic inflammatory diseases (e.g.,
CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
CC fibrils derived from serum amyloid A protein (ApoSSA)); systemic senile
CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
CC fibrils derived from transthyretin (TTR); transmissible spongiform
CC encephalopathies (e.g. Creutzfeld-Jakob disease, Kuru) characterised by
CC prion protein deposits; and beta-2-microglobulin deposits which form as
CC a result of long term haemodialysis treatment. The present sequence
CC represents a human amyloid beta peptide which was conjugated to
CC sheep anti-mouse IgG in an exemplification of the invention.
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 55; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 1 HHQKLVFFAE 10

RESULT 12
AAY30941
ID AAY30941 standard; peptide; 21 AA.
XX
AC AAY30941;
XX
DT 19-OCT-1999 (first entry)
XX
DE Human secretase SEC-alphal peptide fragment.
XX
KW Secretase; hyperforin; treatment; Alzheimer's disease; purification;
KW adhyperforin; St. John's Wort; storage stabile; pharmaceutical;
KW symptom; SEC-alphal; human.
XX
OS Homo sapiens.
XX
PN WO9941220-A1.
XX
PD 19-AUG-1999.
XX
PF 04-FEB-1999; 99WO-EP00737.
XX
PR 13-FEB-1998; 98DE-1005947.
XX
PA (SCHW-) SCHWABE GMBH & CO WILLMAR.
XX

PI Chatterjee SS, Erdelmeier C, Klessing K, Marme D;
PI Schaechtele C;
XX
DR WPI; 1999-508609/42.
XX
PT Hyperforin and adhyperforin isolated from St. John's Wort for
PT treatment of Alzheimers
XX
PS Example 34; Fig 1; 41pp; German.
XX
CC This invention describes novel hyperforin and adhyperforin salts of
CC formula (I): (A-)m (B)p+, where m = 1-3; (A-) = an anion of formula (II);
CC n = 0-1; (B)p+ = an alkali metal ion or an ammonium ion of a salt-forming
CC nitrogen base of formula (III); R1-R3 = H, an optionally branched alkyl,
CC cycloalkyl, bicycloalkyl, tricycloalkyl, alkenyl, alkinyl,
CC heterocycloalkyl, aryl, heteroaryl, arylalkyl or a heteroarylalkyl group,
CC all optionally substituted with one or more hydroxy, alkoxy, aryloxy,
CC alkanoyl, aroyl, carboxy, alkoxycarbamoyl, ureido, amidino, guanidino,
CC cyano, azido, mercapto, alkylthio, alkylsulphoxy, alkylsulphonyl,
CC alkylsulphenyl, aminosulphonyl, fluoro, chloro, bromo, iodo, alkyl or
CC perfluoroalkyl; R1+R2 = together with an N-atom form, together with a
CC N-Atom an azetidin-, pyrrolidin-, pyrrolin-, piperidin-, piperazin-,
CC homopiperazin-, morpholin-, thiomorpholin-, pyridin-, di- or
CC tetra-hydropyridin-, pyrimidin-, pyrazin-, azepin-, dihydroazepin-,
CC oxazepin-, diazepin-, imidazol-, pyrazol-, oxazol- or thiazol-ring,
CC optionally with aliphatic, heteroaliphatic, aromatic or heteroaromatic
CC rings or substituted with hydroxy, alkoxy, aryloxy, alkanoyl, aroyl,
CC carboxy, alkoxycarbamoyl, ureido, amidino, guanidino, cyano, azido,
CC mercapto, alkylthio, alkylsulphoxy, alkylsulphonyl, alkylsulphenyl,
CC aminosulphonyl, fluoro, chloro, bromo, iodo, alkyl or perfluoroalkyl;
CC R4 = H, or an optionally branched alkyl group. The preparation is used to
CC purify the hyperforin and/or adhyperforin content in St. John's Wort
CC extracts. The obtained salts are storage stabile and can be used in
CC pharmaceutical compositions for the treatment of Alzheimer's disease and
CC its symptoms. This sequence represents a fragment of the human secretase
CC SEC-alphal protein which is used to illustrate the method of the
CC invention.
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 55; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 8 HHQKLVFFAE 17

RESULT 13
AAR52569
ID AAR52569 standard; peptide; 24 AA.
XX
AC AAR52569;
XX
DT 16-DEC-1994 (first entry)
XX
DE Alzheimer's disease related immunogen.
XX
KW Alzheimer's disease; senile dementia; immunogen.
XX
OS Synthetic.
XX
PN JP06009693-A.
XX
PD 18-JAN-1994.
XX
PF 23-JAN-1992; 92JP-0031341.
XX
PR 23-JAN-1992; 92JP-0031341.
XX
PA (EIKE) EIKEN KAGAKU KK.
XX
DR WPI; 1994-146876/18.
XX
PT Alzheimer's disease related protein isolated from serum of
PT patient - useful in diagnosis
XX
PS Claim 1; Page 2; 8pp; Japanese.
XX
CC A monoclonal antibody raised against the synthetic peptide AAR52569 as
CC immunogen reacts with a new Alzheimer's disease related protein. The
CC novel protein has a mol.wt. of 20kD (by SDS-PAGE), isoelectric point
CC of ca. 5-7 and is abundant in serum of AD patients.
XX
SQ Sequence 24 AA;

Query Match 100.0%; Score 55; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 14
AAW47229
ID AAW47229 standard; peptide; 26 AA.
XX
AC AAW47229;
XX
DT 22-MAY-1998 (first entry)
XX
DE Beta-amyloid peptide residues 10-35.
XX
KW Screening assay; beta-amyloid peptide; treatment;
KW amyloidosis disease; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5721106-A.
XX
PD 24-FEB-1998.
XX
PF 12-SEP-1994; 94US-0304585.
XX
PR 12-SEP-1994; 94US-0304585.
PR 13-AUG-1991; 91US-0744767.
XX
PA (HARD) HARVARD COLLEGE.
PA (MINU) UNIV MINNESOTA.
XX
PI Maggio JE, Mantyh PW;
XX
DR WPI; 1998-168404/15.
XX
PT New in vitro screening assay for Alzheimer's disease drugs -
PT comprises assessing binding of labelled beta-amyloid peptide to silk
PT sample
XX
PS Claim 8; Columns 31-32; 36pp; English.
XX
CC The present sequence was used in the development of a novel in
CC vitro screening assay for agents capable of affecting the
CC deposition of beta-amyloid peptide (BAP) on tissue. The method
CC comprises contacting a silk sample with labelled BAP, optionally
CC in the presence of a test agent, detecting the amount of label
CC bound to the silk and assessing the effect of the agent on the
CC deposition of BAP. Agents that inhibit binding of BAP to silk are
CC potentially useful for treating amyloidosis diseases, especially
CC Alzheimer's disease.
XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 55; DB 19; Length 26;

```
  Best Local Similarity   100.0%;  Pred. No. 0.0004;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       4 HHQKLVFFAE 13


RESULT 15
AAY33408
ID   AAY33408 standard; peptide; 26 AA.
XX
AC   AAY33408;
XX
DT   03-DEC-1999  (first entry)
XX
DE   Human amyloidogenic A-beta peptide 2.
XX
KW   Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
KW   fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
KW   Down's Syndrome.
XX
OS   Homo sapiens.
XX
PN   WO9941279-A2.
XX
PD   19-AUG-1999.
XX
PF   12-FEB-1999;   99WO-US03231.
XX
PR   13-FEB-1998;   98US-0074658.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Lynn DG,  Meredith SC,  Burkoth TS;
XX
DR   WPI; 1999-561326/47.
XX
PT   Inhibiting amyloid plaque formation in humans suffering from
PT   amyloidosis, Alzheimer's disease or Down's Syndrome -
XX
PS   Claim 22; Page 140; 141pp; English.
XX
CC   This invention describes a novel method for inhibiting amyloid
CC   fibrillogenesis which comprises contacting tissue with a composition
CC   comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
CC   at an end terminal or a side chain, by conjugation to polyethylene
CC   glycol, by conjugation to a second compound and a pharmaceutically
CC   acceptable buffer, solvent or diluent. The methods are used to inhibit
CC   amyloid plaque formation in humans suffering from amyloidosis,
CC   Alzheimer's disease or Down's Syndrome. This sequence represents a
CC   fragment of the beta-amyloid peptide described in the method of the
CC   invention.
XX
SQ   Sequence   26 AA;

  Query Match             100.0%;  Score 55;  DB 20;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.0004;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       4 HHQKLVFFAE 13


RESULT 16
AAY33409
ID   AAY33409 standard; peptide; 27 AA.
XX
AC   AAY33409;
XX
DT   03-DEC-1999  (first entry)
XX
DE   Human amyloidogenic A-beta peptide C-terminal fragment.
XX
KW   Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
KW   fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
KW   Down's Syndrome.
XX
OS   Homo sapiens.
XX
PN   WO9941279-A2.
XX
PD   19-AUG-1999.
XX
PF   12-FEB-1999;   99WO-US03231.
XX
PR   13-FEB-1998;   98US-0074658.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Lynn DG,  Meredith SC,  Burkoth TS;
XX
DR   WPI; 1999-561326/47.
XX
PT   Inhibiting amyloid plaque formation in humans suffering from
PT   amyloidosis, Alzheimer's disease or Down's Syndrome -
XX
PS   Disclosure; Page 141; 141pp; English.
XX
CC   This invention describes a novel method for inhibiting amyloid
CC   fibrillogenesis which comprises contacting tissue with a composition
CC   comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
CC   at an end terminal or a side chain, by conjugation to polyethylene
CC   glycol, by conjugation to a second compound and a pharmaceutically
CC   acceptable buffer, solvent or diluent. The methods are used to inhibit
CC   amyloid plaque formation in humans suffering from amyloidosis,
CC   Alzheimer's disease or Down's Syndrome. This sequence represents the
CC   C-terminal fragment of a PEG-derivatized beta-amyloid peptide described
CC   in the method of the invention.
XX
SQ   Sequence   27 AA;

  Query Match             100.0%;  Score 55;  DB 20;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       5 HHQKLVFFAE 14


RESULT 17
AAP70594
ID   AAP70594 standard; peptide; 28 AA.
XX
AC   AAP70594;
XX
DT   15-APR-1991  (first entry)
XX
DE   Sequence of Alzheimer's amyloid polypeptide (AAP).
XX
KW   Diagnosis; immunologic assay.
XX
OS   Homo sapiens.
XX
PN   US4666829-A.
XX
PD   19-MAY-1987.
XX
PF   15-MAY-1985;   85US-0734660.
XX
PR   15-MAY-1985;   85US-0734660.
XX
PA   (REGC ) UNIV OF CALIFORNIA.
XX
```

PI Glenner GG, Wong CW;
XX
DR WPI; 1987-157148/22.
XX
PT Alzheimer's amyloid polypeptide - used for obtaining antibodies
PT and nucleotide probes for diagnosis of Alzheimer's disease
XX
PS Claim 1; column 11; 8pp; English.
XX
CC Brains obtd. from patients suspected of having Alzheimer's disease
CC and exhibiting extensive cerebrovascular amyloidosis were used for
CC AAP isolation. The AAP can be used to obtain antibodies which can
CC be used as reagents (claimed) in a blood or tissue immunologic
CC assay for the disease. It can also be used to develop a probe
CC (claimed) which can be used in a diagnostic test (claimed).
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 18
AAP90381
ID AAP90381 standard; protein; 28 AA.
XX
AC AAP90381;
XX
DT 01-NOV-1989 (first entry)
XX
DE Synthetic A4 amyloid peptide.
XX
KW Synthetic; A4 amyloid polypeptide; Alzheimer's disease;
KW immunoassays; antibodies.
XX
OS Synthetic.
XX
PN WO8906242-A.
XX
PD 13-JUL-1989.
XX
PF 11-OCT-1988; 88WO-US03590.
XX
PR 08-OCT-1987; 87US-0105751.
XX
PA (MCLE) MCLEAN HOSPITAL CORP; (UYRO) UNIVERSITY OF ROCHESTER.
XX
PI Majocha R, Marotta CA, Zain S;
XX
DR WPI; 1989-220551/30.
XX
PT Antibodies to A4 amyloid polypeptide
PT - used in immunoassays and for imaging of A4 amyloid
PT in Alzheimer's diseased patients.
XX
PS Claim 1; page 27; 30pp; English.
XX
CC Synthetic A4 amyloid polypeptide (see also AAP90382, AAP90383).
CC Used as immunogen, (un)coupled, or to produce antibodies. Used in
CC immunoassays and for imaging of A4 amyloid in Alzheimer's disease.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 19
AAR54702
ID AAR54702 standard; peptide; 28 AA.
XX
AC AAR54702;
XX
DT 15-DEC-1994 (first entry)
XX
DE Beta-amyloid fragment (1-28).
XX
KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9409364-A.
XX
PD 28-APR-1994.
XX
PF 13-OCT-1993; 93WO-US09772.
XX
PR 13-OCT-1992; 92US-0959251.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Strittmatter WJ;
XX
DR WPI; 1994-151484/18.
XX
PT Immobilised beta-amyloid protein or fragments - used in assays
PT for obtaining prods for use in the diagnosis and treatment of
PT disorders such as Alzheimer's disease.
XX
PS Claim 4; Page 28; 49pp; English.
XX
CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp.
CC the peptides given in AAR54702-03) immobilised on a solid support can be
CC used to detect cpds. which bind to BAP. Binding of proteins in
CC human cerebrospinal fluid proteins were shown to bind to beta-
CC amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28)
CC was used as control.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 20
AAR60368
ID AAR60368 standard; peptide; 28 AA.
XX
AC AAR60368;
XX
DT 15-MAR-1995 (first entry)
XX
DE Beta-amyloid (1-28).
XX
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
XX
OS Homo sapiens.
XX
PN WO9417197-A.
XX

PD 04-AUG-1994.
XX
PF 24-JAN-1994; 94WO-JP00089.
XX
PR 25-JAN-1993; 93JP-0010132.
PR 05-FEB-1993; 93JP-0019035.
PR 16-NOV-1993; 93JP-0286985.
PR 28-DEC-1993; 93JP-0334773.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kitada C, Odaka A, Suzuki N;
XX
DR WPI; 1994-264110/32.
XX
PT Antibodies recognising specific parts of beta-amyloid - can be
PT used for diagnosis of diseases implicating beta-amyloid, such as
PT Alzheimer's disease
XX
PS Claim 7; Page 84; 116pp; Japanese.
XX
CC Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
CC from the C-terminal portion. The antibodies are useful for assaying
CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
CC disease.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 21
AAR64170
ID AAR64170 standard; peptide; 28 AA.
XX
AC AAR64170;
XX
DT 03-AUG-1995 (first entry)
XX
DE A4-O(1-28) a partial beta amyloid peptide.
XX
KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW Down's syndrome; A4-O(1-28).
XX
OS Synthetic.
XX
PN WO9428412-A.
XX
PD 08-DEC-1994.
XX
PF 27-MAY-1994; 94WO-US05809.
XX
PR 28-MAY-1993; 93US-0069010.
XX
PA (MIRI-) MIRIAM HOSPITAL.
XX
PI Majocha RE, Marotta CA;
XX
DR WPI; 1995-023013/03.
XX
PT Amyloid binding composition comprising labelled amyloid protein
PT and carrier - useful for in vivo imaging of amyloid deposits, for
PT diagnosing Alzheimer's disease and Down's Syndrome.
XX
PS Example 1; Page 23; 58pp; English.
XX
CC AAR64170, the A4-O(1-28) polypeptide is the first 28 amino acids of the
CC 4.2 kD peptide deriv. from senile plaque cores of an AD (Alzheimer's
CC disease) brain, known as beta amyloid. A4-O has strong aggregation
CC properties, and binds to itself strongly. This peptide is used to obtain
CC and select beta amyloid proteins that can be used for in vivo imaging
CC of amyloid deposits and hence diagnosis of an amyloidosis-associated
CC disease, such as AD or Down's syndrome. AAR64165 shows the generic
CC sequence of the amyloid protein for generation of variants.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 22
AAR64171
ID AAR64171 standard; peptide; 28 AA.
XX
AC AAR64171;
XX
DT 03-AUG-1995 (first entry)
XX
DE A4-P(1-28) a partial beta amyloid peptide.
XX
KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW Down's syndrome; A4-P(1-28).
XX
OS Synthetic.
XX
PN WO9428412-A.
XX
PD 08-DEC-1994.
XX
PF 27-MAY-1994; 94WO-US05809.
XX
PR 28-MAY-1993; 93US-0069010.
XX
PA (MIRI-) MIRIAM HOSPITAL.
XX
PI Majocha RE, Marotta CA;
XX
DR WPI; 1995-023013/03.
XX
PT Amyloid binding composition comprising labelled amyloid protein
PT and carrier - useful for in vivo imaging of amyloid deposits, for
PT diagnosing Alzheimer's disease and Down's Syndrome.
XX
PS Example 3; Page 23; 58pp; English.
XX
CC AAR64171, the A4-P(1-28) polypeptide is deriv. from vascular amyloid of
CC the AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of
CC the 28 amino acids are different from the A4-O(1-28) peptide shown in
CC AAR64170. A4-O has strong aggregation properties, and binds to itself
CC strongly. It is used to obtain and select beta amyloid proteins that can
CC be used for in vivo imaging of amyloid deposits and hence diagnosis of
CC an amyloidosis-associated disease, such as AD or Down's syndrome.
CC AAR64165 shows the generic sequence of the amyloid protein for generation
CC of variants.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;

```
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 23
AAR64172
ID   AAR64172 standard; peptide; 28 AA.
XX
AC   AAR64172;
XX
DT   03-AUG-1995  (first entry)
XX
DE   A4-B(1-28) a partial beta amyloid peptide.
XX
KW   beta amyloid protein; mutant; variant; detection; amyloid deposition;
KW   diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW   Down's syndrome; A4-B(1-28).
XX
OS   Synthetic.
XX
PN   WO9428412-A.
XX
PD   08-DEC-1994.
XX
PF   27-MAY-1994;   94WO-US05809.
XX
PR   28-MAY-1993;   93US-0069010.
XX
PA   (MIRI-) MIRIAM HOSPITAL.
XX
PI   Majocha RE,  Marotta CA;
XX
DR   WPI; 1995-023013/03.
XX
PT   Amyloid binding composition comprising labelled amyloid protein
PT   and carrier - useful for in vivo imaging of amyloid deposits, for
PT   diagnosing Alzheimer's disease and Down's Syndrome.
XX
PS   Example 3; Page 23; 58pp; English.
XX
CC   AAR64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of
CC   the AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of
CC   the 28 amino acids are different from the A4-O(1-28) peptide shown in
CC   AAR64170. A4-O has strong aggregation properties, and binds to itself
CC   strongly. It is used to obtain and select beta amyloid proteins that can
CC   be used for in vivo imaging of amyloid deposits and hence diagnosis of
CC   an amyloidosis-associated disease, such as AD or Down's syndrome.
CC   AAR64165 shows the generic sequence of the amyloid protein for generation
CC   of variants.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 16;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 24
AAR64164
ID   AAR64164 standard; peptide; 28 AA.
XX
AC   AAR64164;
XX
DT   02-AUG-1995  (first entry)
XX
DE   Generic beta amyloid protein variant.
XX
KW   generic sequence; beta amyloid protein; mutant; variant; detection;
KW   amyloid deposition; diagnosis; amyloidosis associated disease;
KW   Alzheimer's disease; Down's syndrome.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 11
FT                   /note= "Glu or Gln"
FT   Misc-difference 27
FT                   /note= "Ser or Asn"
FT   Misc-difference 28
FT                   /note= "Ala or Lys"
XX
PN   WO9428412-A.
XX
PD   08-DEC-1994.
XX
PF   27-MAY-1994;   94WO-US05809.
XX
PR   28-MAY-1993;   93US-0069010.
XX
PA   (MIRI-) MIRIAM HOSPITAL.
XX
PI   Majocha RE,  Marotta CA;
XX
DR   WPI; 1995-023013/03.
XX
PT   Amyloid binding composition comprising labelled amyloid protein
PT   and carrier - useful for in vivo imaging of amyloid deposits, for
PT   diagnosing Alzheimer's disease and Down's Syndrome.
XX
PS   Claim 3; Page 42; 58pp; English.
XX
CC   AAR64164 shows the generic amino acid sequence of a variant beta amyloid
CC   protein. The protein binds amyloid and is useful for in vivo imaging of
CC   amyloid deposits and hence diagnosis of an amyloidosis-associated
CC   disease, such as Alzheimer's disease or Down's syndrome. AAR64165-69
CC   show specifc variants generated from this generic sequence with addition
CC   amino acids.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 16;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 25
AAW01413
ID   AAW01413 standard; Protein; 28 AA.
XX
AC   AAW01413;
XX
DT   20-JAN-1997  (first entry)
XX
DE   Beta/A4-amyloid peptide residues 1-28.
XX
KW   Beta/A4-amyloid peptide; tissue plasminogen activator;
KW   Alzheimer's disease; stimulation; investigation; pathogenesis;
KW   hereditary cerebral haemorrhage with amyloidosis-Dutch type;
KW   control; cerebral amyloid angiopathy; cerebral; haemorrhage;
KW   hemorrhage.
XX
OS   Homo sapiens.
XX
PN   WO9615799-A1.
XX
```

PD 30-MAY-1996.
XX
PF 22-NOV-1995; 95WO-US15007.
XX
PR 22-NOV-1994; 94US-0347144.
XX
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Anderson S;
XX
DR WPI; 1996-268332/27.
XX
PT Use of agents which bind beta-amyloid peptide - for diagnosis,
PT prevention and treatment of vascular damage caused by amyloid
PT deposits, partic. in haemorrhaging and Alzheimer's disease
XX
PS Example 1; Fig 1; 52pp; English.
XX
CC To investigate the effects of beta-amyloid peptide (BAP) on
CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
CC One peptide contained 42 amino acids and corresp. to the full
CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
CC (HCHWA-D), respectively. In an assay to determine the effect of
CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)
CC gave 1st order rate constant of activation (k(app)) values of
CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for nill
CC and fibrinogen controls. The results demonstrate that the BAP are
CC able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
CC angiopathy related cerebral haemorrhage.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 26
AAY39805
ID AAY39805 standard; peptide; 28 AA.
XX
AC AAY39805;
XX
DT 29-NOV-1999 (first entry)
XX
DE Beta-amyloid protein, Beta/A4 amyloid (1-28).
XX
KW Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
KW long-standing inflammation; malignancy; Familial Mediterranean Fever;
KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
KW Creutzfeldt-Jakob disease; Gerstmann Strausiler Syndrome;
KW subacute spongiform encephalopathy; therapy.
XX
OS Homo sapiens.
XX
PN US5958883-A.
XX
PD 28-SEP-1999.
XX
PF 05-JUN-1995; 95US-0461216.
XX
PR 23-OCT-1992; 92US-0969734.
PR 23-SEP-1992; 92US-0950417.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Snow AD;
XX
DR WPI; 1999-561062/47.
XX
PT Peptides of 6-8 amino acids useful for treating or preventing
PT amyloidosis -
XX
PS Disclosure; Column 67-68; 83pp; English.
XX
CC This sequence represents a fragment of the beta-amyloid protein. The
CC invention relates to a method for treating or preventing a form of
CC amyloidosis, including Alzheimer's disease using this sequence. The
CC compositions may be useful for treating or preventing the amyloidosis
CC associated with long-standing inflammation, various forms of malignancy
CC (including B-cell type malignancies), Familial Mediterranean Fever,
CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
CC Creutzfeldt-Jakob disease, Gerstmann Strausiler Syndrome, kuru, scrapie
CC and other subacute spongiform encephalopathies.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 20; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 27
AAW81467
ID AAW81467 standard; peptide; 28 AA.
XX
AC AAW81467;
XX
DT 28-JAN-1999 (first entry)
XX
DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).
XX
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
OS Synthetic.
XX
PN US5840838-A.
XX
PD 24-NOV-1998.
XX
PF 29-FEB-1996; 96US-0609090.
XX
PR 29-FEB-1996; 96US-0609090.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
XX
DR WPI; 1999-034120/03.
XX
PT Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
XX
PS Claim 5; Columns 9-10; 14pp; English.
XX
CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated

CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC ''evaporative deposition'' in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation..
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 20; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 28
AAB91783
ID AAB91783 standard; Peptide; 28 AA.
XX
AC AAB91783;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:959.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 507; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 29
AAB91789
ID AAB91789 standard; Peptide; 28 AA.
XX
AC AAB91789;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:965.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 509; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

```
XX
SQ   Sequence   28 AA;

  Query Match            100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22


RESULT 30
AAB91800
ID   AAB91800 standard; Peptide; 28 AA.
XX
AC   AAB91800;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Amyloid beta-protein fragment peptide SEQ ID NO:976.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 513; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   28 AA;

  Query Match            100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22


RESULT 31
AAB91816
ID   AAB91816 standard; Peptide; 28 AA.
XX
AC   AAB91816;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Amyloid beta-protein fragment peptide SEQ ID NO:992.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 519; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   28 AA;

  Query Match            100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22
```

```
RESULT 32
AAB91827
ID   AAB91827 standard; Peptide; 28 AA.
XX
AC   AAB91827;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Amyloid beta-protein fragment peptide SEQ ID NO:1003.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 523; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 33
AAB49396
ID   AAB49396 standard; peptide; 28 AA.
XX
AC   AAB49396;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Human amyloid peptide protein fragment SEQ ID NO: 11.
XX
KW   Human; immunogenic peptide; immune response; monophosphoryl lipid A;
KW   antigen; infection; cancer; amyloid deposition.
XX
OS   Homo sapiens.
XX
PN   WO200069456-A2.
XX
PD   23-NOV-2000.
XX
PF   12-MAY-2000; 2000WO-US13156.
XX
PR   13-MAY-1999;   99US-0133963.
XX
PA   (AMCY ) AMERICAN CYANAMID CO.
XX
PI   Hagen M;
XX
DR   WPI; 2001-024946/03.
XX
PT   Antigenic composition having an antigen (e.g. viral protein) and an
PT   adjuvant, useful for enhancing humoral and cellular immune response in
PT   a host or as a prophylaxis against virus, bacterium, parasite, cancer
PT   cell or allergen  -
XX
PS   Disclosure; Page 40; 129pp; English.
XX
CC   The present invention provides an antigenic composition comprising an
CC   antigen with a 3-O-deacylated monophosphoryl lipid A or monophosphoryl
CC   lipid A adjuvant. The presence of the adjuvant causes an increased immune
CC   response. The antigen may be from a pathogenic bacterium, fungus, virus
CC   or parasite, a cancer cell, an allergen or from amyloid peptide protein.
CC   The composition can be used in the prevention and treatment of infection,
CC   cancer and diseases caused by amyloid deposition. It is particularly
CC   useful against HIV, Neisseria gonorrhoeae and respiratory syncytial
CC   virus.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 34
AAB35590
ID   AAB35590 standard; peptide; 28 AA.
XX
AC   AAB35590;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
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PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match           100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22


RESULT 35
AAB35591
ID   AAB35591 standard; peptide; 28 AA.
XX
AC   AAB35591;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone D1N B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match           100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HHQKLVFFAE 10
          ||||||||||
Db     13 HHQKLVFFAE 22


RESULT 36
AAB35592
ID   AAB35592 standard; peptide; 28 AA.
XX
AC   AAB35592;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone E3Q B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match           100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 37
AAB35593
ID   AAB35593 standard; peptide; 28 AA.
XX
AC   AAB35593;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone R5Q B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match            100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 38
AAB35594
ID   AAB35594 standard; peptide; 28 AA.
XX
AC   AAB35594;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone H6Q B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match            100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 39
AAB35595
ID   AAB35595 standard; peptide; 28 AA.
XX
AC   AAB35595;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone D7Q B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
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XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 40
AAB35596
ID   AAB35596 standard; peptide; 28 AA.
XX
AC   AAB35596;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone E11Q B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 41
AAB36201
ID   AAB36201 standard; peptide; 28 AA.
XX
AC   AAB36201;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone D23Q B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 42
```

```
AAB36202
ID   AAB36202 standard; peptide; 28 AA.
XX
AC   AAB36202;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human clone K28Q B(1-28) amyloid B peptide.
XX
KW   Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW   acute cardiovascular disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6136548-A.
XX
PD   24-OCT-2000.
XX
PF   02-SEP-1999;   99US-0388890.
XX
PR   26-JUL-1996;   96US-0686959.
PR   22-NOV-1994;   94US-0347144.
PR   22-NOV-1995;   95WO-US15007.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Anderson S;
XX
DR   WPI; 2001-030939/04.
XX
PT   Identifying mutant tissue-type plasminogen activator (t-PA) for
PT   improving thrombolytic therapy or treating vascular hemorrhaging, by
PT   determining whether t-PA binds to fibrin but not to a beta amyloid
PT   peptide -
XX
PS   Example 3; Column 26; 23pp; English.
XX
CC   The present invention describes a method for identifying mutant
CC   derivatives of tissue-type plasminogen activator, which involves
CC   determining whether or not they bind to beta-amyloid peptides and fibrin.
CC   Mutants will only bind to the latter. These mutants are useful in
CC   improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC   and in the treatment of acute cardiovascular disease, which may be caused
CC   by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 55;  DB 22;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 43
AAW81468
ID   AAW81468 standard; peptide; 30 AA.
XX
AC   AAW81468;
XX
DT   28-JAN-1999  (first entry)
XX
DE   Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).
XX
KW   Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW   research; neurotoxicity; free-radical; glutamine synthetase.
XX
OS   Synthetic.
XX
PN   US5840838-A.
XX
PD   24-NOV-1998.
XX
PF   29-FEB-1996;   96US-0609090.
XX
PR   29-FEB-1996;   96US-0609090.
XX
PA   (KENT ) UNIV KENTUCKY RES FOUND.
XX
PI   Aksenov M,  Butterfield DA,  Carney JM,  Hensley K;
XX
DR   WPI; 1999-034120/03.
XX
PT   Process for treating synthetic amyloid beta peptides - by organic
PT   solvent treatment, useful for studying neurotoxicity
XX
PS   Claim 5; Columns 9-10; 14pp; English.
XX
CC   Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC   peptides. The invention provides a process for treating a synthetic
CC   Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC   solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC   sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC   acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC   solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC   ''evaporative deposition'' in 5-10 minutes. Synthetic amyloid beta
CC   peptides are useful as research tools for studying neurotoxicity
CC   resulting from Abeta peptide -enhanced free-radical production. The
CC   treatment increases the activity of the synthetic Abeta peptides in tests
CC   to determine free-radical generating capacity and glutamine synthetase
CC   inactivation.
XX
SQ   Sequence   30 AA;

  Query Match             100.0%;  Score 55;  DB 20;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.00047;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22


RESULT 44
AAB84430
ID   AAB84430 standard; peptide; 32 AA.
XX
AC   AAB84430;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Partial sequence of a human beta-amyloid precursor protein.
XX
KW   Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
KW   vaccine.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "pyroglutamate"
XX
PN   WO200142306-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33203.
XX
PR   08-DEC-1999;   99US-0169687.
XX
PA   (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
XX
PI   Chain B;
XX
```

DR WPI; 2001-381648/40.
XX
PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
PT epitope from naturally occurring internal peptide cleavage product
PT (such as beta amyloid peptide) of a precursor protein, joined to T cell
PT epitope -
XX
PS Claim 3; Page 42-43; 47pp; English.
XX
CC The present sequence represents a partial sequence of a human
CC beta-amyloid precursor protein (APP). The peptide is used to create
CC chimeric peptides of the invention. The chimeric peptides contain a N-
CC or C-terminal end-specific B cell epitope from a naturally occurring
CC internal peptide cleavage product of a precursor or mature protein, as
CC a free N- or C-terminus, joined to a T cell epitope, with or without a
CC spacer amino acid residue. Chimeric peptides comprising betaAPP peptides
CC slow down, reduce or prevent the accumulation of amyloid beta peptide in
CC the extracellular space, interstitial fluid and cerebrospinal fluid of
CC the brain, and aggregation into senile amyloid deposits or plaques. They
CC also block the interaction of amyloid beta peptides with other molecules
CC that contribute the neurotoxicity of amyloid beta. The chimeric peptides
CC are useful for immunizing humans against the free N- or C-terminus of
CC an internal self peptide cleavage product (e.g. APP peptide) derived from
CC a precursor protein or a mature protein. The internal peptide cleavage
CC product is the self molecule of the mammal.
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 55; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 3 HHQKLVFFAE 12

RESULT 45
AAW81469
ID AAW81469 standard; peptide; 33 AA.
XX
AC AAW81469;
XX
DT 28-JAN-1999 (first entry)
XX
DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).
XX
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
OS Synthetic.
XX
PN US5840838-A.
XX
PD 24-NOV-1998.
XX
PF 29-FEB-1996; 96US-0609090.
XX
PR 29-FEB-1996; 96US-0609090.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
XX
DR WPI; 1999-034120/03.
XX
PT Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
XX
PS Claim 5; Columns 9-10; 14pp; English.
XX
CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC ''evaporative deposition'' in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
XX
SQ Sequence 33 AA;

Query Match 100.0%; Score 55; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

RESULT 46
AAW47228
ID AAW47228 standard; peptide; 35 AA.
XX
AC AAW47228;
XX
DT 22-MAY-1998 (first entry)
XX
DE Beta-amyloid peptide residues 1-35.
XX
KW Screening assay; beta-amyloid peptide; treatment;
KW amyloidosis disease; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5721106-A.
XX
PD 24-FEB-1998.
XX
PF 12-SEP-1994; 94US-0304585.
XX
PR 12-SEP-1994; 94US-0304585.
PR 13-AUG-1991; 91US-0744767.
XX
PA (HARD) HARVARD COLLEGE.
PA (MINU) UNIV MINNESOTA.
XX
PI Maggio JE, Mantyh PW;
XX
DR WPI; 1998-168404/15.
XX
PT New in vitro screening assay for Alzheimer's disease drugs -
PT comprises assessing binding of labelled beta-amyloid peptide to silk
PT sample
XX
PS Claim 8; Columns 31-32; 36pp; English.
XX
CC The present sequence was used in the development of a novel in
CC vitro screening assay for agents capable of affecting the
CC deposition of beta-amyloid peptide (BAP) on tissue. The method
CC comprises contacting a silk sample with labelled BAP, optionally
CC in the presence of a test agent, detecting the amount of label
CC bound to the silk and assessing the effect of the agent on the
CC deposition of BAP. Agents that inhibit binding of BAP to silk are
CC potentially useful for treating amyloidosis diseases, especially
CC Alzheimer's disease.
XX
SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 19; Length 35;

Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22
```

RESULT 47
AAW89357
ID AAW89357 standard; peptide; 35 AA.
XX
AC AAW89357;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-6-40.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Claim 5; Column 81-82; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 HHQKLVFFAE 10
           ||||||||||
Db       8 HHQKLVFFAE 17
```

RESULT 48
AAW89359
ID AAW89359 standard; peptide; 35 AA.
XX
AC AAW89359;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-1-25,31-40 (Delta26-30).
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Claim 7; Column 81-82; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 HHQKLVFFAE 10
           ||||||||||
Db      13 HHQKLVFFAE 22
```

RESULT 49
AAW89361
ID AAW89361 standard; peptide; 35 AA.
XX
AC AAW89361;
XX

DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-1-5,11-40 (Delta6-10).
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
PS Claim 9; Column 83-84; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 8 HHQKLVFFAE 17

RESULT 50
AAW81471
ID AAW81471 standard; peptide; 36 AA.
XX
AC AAW81471;
XX
DT 28-JAN-1999 (first entry)
XX
DE Synthetic amyloid beta (Abeta) peptide 6 (residues 1-36).
XX
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
OS Synthetic.
XX
PN US5840838-A.
XX
PD 24-NOV-1998.
XX
PF 29-FEB-1996; 96US-0609090.
XX
PR 29-FEB-1996; 96US-0609090.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
XX
DR WPI; 1999-034120/03.
XX
PT Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
XX
PS Claim 5; Columns 11-12; 14pp; English.
XX
CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC ''evaporative deposition'' in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 55; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAE 10
||||||||||
Db 13 HHQKLVFFAE 22

Search completed: October 29, 2002, 09:24:07
Job time : 33 secs